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                                                                                                                   4, 2005, 08:37:33 ; Search time 78.7907 Seconds (without alignments) 68.722 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                               2105692 seqs, 386760381 residues
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Gapop 10.0 , Gapext
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AAM04355 Aaw04355 Chimaeric AAR97413 Aar97413 Streptoco AAR97414 Atreptoco AdG62865 Streptoco ADG62863 AdG62865 Streptoco ADG62863 AdG62865 Streptoco ADG62863 AdW04352 Chimaeric AAR97412 Aav97412 Arspring AAR9741 Aar9741 Arreptoco AAR9741 Aar9741 Arreptoco AAR97426 Aar9741 Arreptoco AAR97426 Aar9741 Arreptoco AAR07486 Aar9741 Arreptoco AAW14350 Aaw14350 Chimaeric AAB00551 Abp80951 N. gonorr AAY74876 Aay74876 Aab01122 AAR50999 Recombina AAR50999 Recombina AAB03121 S. pyogen	ALIGNMENTS	20 AA.		occus M protein.	treptococci, antibody, human heart tissue; ; diagnosis.					INST MEDICAL RES.			riges at least one B-cell epitope from useful in vaccine for streptococcal infections.	ish.	beta-haemolytic streptococc beta-haemolytic streptococc the peptide shown, peptide 1 , where an antibody reactiv strive to human heart tissue,	ie 101 inducting numeral rumunity against tibodies to the peptide are useful in . (Updated on 25-MAR-2003 to correct PN
201128 821228 122222 122128 12222 1222 12222 12222 12222 12222 12222 12222 12222 12222 12222 12222 122		; pèptide;	(revised) (first entry)	from Streptococcus M	haemolytic stre oral immunity; o			93WO-AU000131	92AU-00001800	COUNCIL QUEENSLAND	orn S;	44.	peptide - comprises ccal M-protein, usef	57pp; English	comprises an N-termina M protein of group A E type 5 M-protein). ? least 1 B cell epitope is only minimally readent is a vacche for	in a vacci ections. Ar infections
88888848 7888888848 78888884 888884 8888 8888 8888 8888 8888 8888 8888 8888		standard;	(rev (fir		haem oral		:		92	CIL 0	Pruksakorn	51655/	ptide 1 M-p	Je 38;		userur cal infe cal such :
4 4 0 00 00 00 00 00 00 00 00 00 00 00 00 0		1 43 AR43343 AB43343	15-MAR-2003 11-MAY-1994	B cell epitope	roup A b accine;	Synthetic.	WO9321220-A1 28-OCT-1993.	30-MAR-1993;	08-APR-1992;	(coun-) coun	Good MF, Pr	WPI; 1993-35	ynthetic treptoco	Claim 7; Page	The peptide or region of the 337-492 of the comprises at cell epitope or contractions.	peptide is use streptococcal diagnosis of s field.)
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		343													3888888	

100.0%; Score 64; DB 2; Length 20;

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Sequence 20 Query Match

field.)

Streptoco Type-6 M-

Streptoco S. pyogen S pyrogen Chimaeric Streptoco Chimaeric

483 484 539 128 28

Matchea

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This sequence represents a fragment of a Streptococcus group A protein. This sequence was used to test the acryloylated peptide polymer of the invention. The peptide polymers are used to raise an immune response to a peptide epitope (such as this sequence), and also as diagnostic tools. Polymers (molecular wt. >600 kDa.) can be prepared with virtually any number of the same or different epitopes by a method that allows purification of the individual determinants, avoids errors inherent in long sequential syntheses in which protected peptide fragments are not used, thus avoiding solubility and purification problems. Multiple copies of many different peptide epitopes may be incorporated into a single polymeric structure to allow utilisation of the range of T cell epitopes required for outbrend populations in conjunction with epitopes required for outbrend populations in conjunction with epitopes significant advance in synthetic vaccine technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acryloylated peptide polymers - useful for synthetic vaccine technology, for raising an immune response to peptide epitope and as diagnostic tool.
                                                                                                                                                                                                                                                                            Acryloylated peptide polymer; immune response; peptide epitope; synthetic vaccine; enzymatically cleavable site.
                                                                                                                                                                                                                                                                                                                                                                                                                           note= "linked to acryloylated peptide polymer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 64; DB 2; Length 20; 100.0%; Pred. No. 0.0019; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                       Streptococcus group A protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 20; 77pp; English.
                                                                                                           AAW69281 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-AU000076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97AU-00005071.
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    7 ASREAKKQVEKALE 20
                                                                                                                                                                                           29-OCT-1998 (first entry)
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                     AAW69281;
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                                                                    RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present peptide is the Streptococcal M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)), used in the construction of a novel chimaeric peptide (CP). The CP comprises a B-cell conformational epitope from within the present peptide, inserted into a peptide (AAR97395). The 2D oppide has a similar conformation, enabling the epitope to be presented in an immunologically active conformation. The CP can be used in a novel detection/mapping process, e.g. to and the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against typ. A Streptococci, Ab raised against the CP can be used for immunotherapy and diagnosis, while the CP can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines and for determn. of minimal epitope(s) or for mapping amphipathic helices.
                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcal, M protein, peptide; p145; chimaeric; chimeric; B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper; detection; mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
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                          Gaps
                                                                                                                                                                                                                                                                                                                                                                  Streptococcal M protein peptide p145, for use in chimaeric peptide.
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                        Indels
    Pred. No. 0.0019;
Mismatches 0;
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                        0; Mismatches
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                                                                                                                                                                                                                 AAR97390 standard; peptide; 20 AA.
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100.08;
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    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
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02-DEC-1996
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AAR97390;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                               T helper cell epitope, B cell epitope, Antibacterial, Antiulcer, Antinfertility; Vaccine, antibody.
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                                                                                                 Immunogenic lipopeptide of the invention #101.
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                                                                                                                                                                                                                                                                                                                                                  (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 29; SEQ ID NO 101; 194pp; English.
ADK00565 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK00571 standard; peptide; 45 AA.
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                                                                                                                                                                                                                                                                                                                 12-AUG-2002; 2002US-0402838P
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                                                                                                                                                                                                                                                                                                                                                                                    Zeng W;
                                                                                                                                                                                                               WO2004014956-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   Jackson D,
                                                                                                                                                                                Synthetic.
                                ADK00565;
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Matches
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The present invention realtes to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid sequence of Thelper cell epitope and B cell epitope, where amino acid sequences are different, and internal lysine residues or internal lysine analog residues for covalent attachment of each of lipid moieties through kegr; amino group or terminal side chain group of lysine or lysine analog. The peptides are useful in eliciting the production of antibody against an antigent B cell epitope in a subject, and are useful for antibody production, synthetic vaccine production, diagnostic method employing antibodies and antibody ligands and immunotherapy for production of antibody against antigenic B cell epitope. The present sequence represents a novel immunogenic lipopeptide comprising T helper
                                                                                                                                                                                                                                                                              Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T helper cell epitope, B cell epitope, Antibacterial, Antiulcer, Antinfertility; Vaccine, antibody.
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                                                                                                                                                                                     (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                            Claim 39; SEQ ID NO 107; 194pp; English.
Antiinfertility; Vaccine; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK00569 standard; peptide; 46 AA.
                                                                                                                           12-AUG-2003; 2003WO-AU001018.
                                                                                                                                                        12-AUG-2002; 2002US-0402838P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASREAKKQVEKALE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASREAKKOVEKALE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                   WPI; 2004-238735/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and B cell epitopes.
                                                                                                                                                                                                                    Jackson D, Zeng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004014956-A1.
                                                             WO2004014956-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-2004
                                                                                          19-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-2004
                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK00569;
                                                                                                                                                                                                                                                                                                                                  antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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12-AUG-2002; 2002US-0402838P

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WPI; 2004-238735/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zeng W;
                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004014956-A1.
                                                                                                                                                                                                           Sequence 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jackson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                     ADK00570;
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen.
                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                        The present invention realtes to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid agequence of Thalper cell epitope and B call epitope, where amino acid sequences are different, and internal lysine residues or internal lysine analog residues for covalent attachment of each of lipid moieties through kegr; amino group or terminal side chain group of lysine or lysine analog. The peptides are useful in eliciting the production of antibody against an antigenic B cell epitope in a subject, and are useful for antibody production, synthetic vaccine production, diagnostic method employing antibodies and antibody ligands and immunotherapy for veterinary and human medicine. The method efficiently elicits the production of antibody against antigenic B cell epitope. The present sequence represents a novel immunogenic lipopeptide comprising T helper
                                                                              H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel lipopeptide comprising polypeptide having amino acid sequence of 'helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus
                                                                            Novel lipopeptide comprising polypeptide having amino acid sequence of helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T helper cell epitope, B cell epitope, Antibacterial, Antiulcer, Antinfertility; Vaccine, antibody.
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                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 64; DB 8; Length 46; 100.0%; Pred. No. 0.0047; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic lipopeptide of the invention #108.
         (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES
                                                                                                                                    Claim 39; SEQ ID NO 105; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK00572 standard; peptide; 46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-2003; 2003WO-AU001018.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                                                                B cell epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-238735/22.
                                                    WPI; 2004-238735/22
                                 Zeng W;
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                                                                                                                                                                                                                                                                                                                                       Sequence 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
                               Jackson D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jackson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK00572;
                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                               antigen.
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Matches
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FILLLEY
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                                                                          The present invention realtes to a lipopeptide comprising polypeptide conjugated to lipid molecies, where polypeptide contains amino acid sequence of T helper cell epitope and B cell epitope, where amino acid sequences are different, and internal lyaine residues or internal lysine analog residues for covalent attachment of each of lipid molecies through tegy; amino group or terminal side chain group of lysine or lysine analog. The peptides are useful in elicting the production of antibody antibody production, synthetic vaccine production, diagnostic method employing antibody production; synthetic vaccine production, diagnostic method employing antibodies and antibody ligands and immunotherapy for production of antibody against an etilogenic B cell epitope. The method efficiently elicits the production of antibody against antigenic B cell epitope. The present sequence represents a novel immunogenic lipopeptide comprising T helper and B cell epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention realtes to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid sequence of T helper cell epitope and B cell epitope, where amino acid sequences are different, and internal lyaine residues or internal lyaine analog residues for covalent attachment of each of lipid moieties through each; amino group or terminal side chain group of lyaine analog. The peptides are useful in eliciting the production of antibody against an antigenic B cell epitope in a subject, and are useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 64; DB 8; Length 46; 100.0%; Pred. No. 0.0047; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 39; SEQ ID NO 106; 194pp; English.
Claim 39; SEQ ID NO 108; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK00570 standard; peptide; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-2003; 2003WO-AU001018
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Multivalent hybrid M protein; M5; group A streptococcus; serotype; immunogenic; sero-specific antibody; streptococcal infection; cross reactivity; vaccine; acute rheumatic fever; ARF; rheumatic heart disease; streptococcal pharyngitis; strep throat;

Streptococcus pyogenes.

pneumonia.

US6063386-A. 16-MAY-2000,

C-terminus of Streptococcus pyogenes M protein M5.

(first entry)

10-OCT-2000

AAB03118;

AAB03118 standard; protein; 236 AA.

RESULT 10

AAB0311

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antibody production, synthetic vaccine production, diagnostic method employing antibodies and antibody ligands and immunotherapy for veterinary and human medicine. The method efficiently elicits the production of antibody against antigenic B cell epitope. The present sequence represents a novel immunogenic lipopeptide comprising T helper and B cell epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant streptococcal M protein DNA and viral vector - for production of poxviridae vaccines in treatment of vaccinia, fowlpox etc.
                                                                                                                                                                       Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcal M protein; M'6 protein; vaccinia virus; fowlpox virus; poxviridiae vaccine; streptococcal pharangytis.
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                                                                                                                                  100.0%; Score 64; DB 8; Length 47; 100.0%; Pred. No. 0.0048; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.026;
M*matches 0; Indels
                                                                                                                                                                                                                                                                                                          AAR10221 standard; protein; 234 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-00369118.
90US-00540586.
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                                                                                                                                                                                                                  1 ASREAKKOVEKALE 14
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcal M6' protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYRQ ) UNIV ROCKEFELLER. (UYOR-) UNIV OREGON STATE.
                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fischetti VA, Kruby DE;
                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-022236/03.
                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ10244
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                                                                                                         Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-1989;
19-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
26-MAR-1991
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                                                                                                                                                                    Matches
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(UYTE-) UNIV TENNESSEE RES CORP.

Dale JB;

Lederer JW,

92US-00945954.

16-SEP-1992;

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                                                                                                                     New immunogenic recombinant hybrid M protein comprising amino-terminal peptide fragments of streptococcal M protein useful as vaccine against rheumatic fever and infections leading to rheumatic fever.
                                                                                                                                                                                                                                                                            Gapa
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                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                   Query Match

100.0%; Score 64; DB 3;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                      Disclosure; Col 45-46; 62pp; English.
                                                                                                             WPI; 2000-364475/31.
                                                                                                                                                                                                                                                           Sequence 236 AA;
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Gaps

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98

14

1 ASREAKKQVEKALE ASREAKKOVEKALE

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Conservative

Local Similarity nes 14; Conserv

Query Match Best Loca Matches

2; Length 234;

Thu Aug

AAR50228;

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us-10-706-275-1.rag

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The inventors claim a protein prod. by a strain of Gp.A Streptococci. The protein has the AA sequence of protein H but lacks at least some part of the C and D regions (responsible for binding albumin), esp. it lacks the whole of these regions and extends for AA1 to AA158. Compared with matural protein H, it is more specific and may be used as part of a kit for the binding, separation and identification of human IgG. The same sequences appear in WO9119741. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New IgG binding proteins H' lacking an albumin binding sequence in purificn. of excess IgG from blood and to diagnose autoimmune
                                                                                                                    Protein H; immunoglobulin G; IgG; antibody; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 64; DB 2; Length 281; 100.0%; Pred. No. 0.032; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cooney J, Bjorck L;
                                                                                  Sequence encoded by truncated M1 gene.
                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR50229 standard; protein; 284 AA.
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                                                                                                                                                                                                       1. .28
/label= p16M1
29. .70
/label= C1
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                                                                                                                                                                                                                                                                      71. .112
/label= C2
113. .155
/label= C3
/label= C4
177. .281
/label= D
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                                                (first entry)
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmidt KH, Akesson P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-024366/03.
N-PSDB; AAQ20292.
                                                                                                                                                       Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                WO9119740-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-1991.
                              27-AUG-2003
15-APR-1992
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AAR20128
                                                                                                                                                                                                       Region
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The surface M protein of Group A streptococi is the major virulence factor and protective antigen of these organisms. However, there are a rremembous number of M protein serovypes. The invention provides recombinant M protein antigens comprising a gene encoding a carrier protein and an NH2 or COOH terminal M protein fragment carrying one or more epitopes. The carrier may be the B subunit of E.coli labile toxinn (LT-B) or the C-repeat portion of a streptococcal M protein. For example, AAQ45160/R5028 comprises an antigen which is an MS hapten fragment of terminal half of MS. The carrier includes 2.5 C-repeats, which each commence with the tetrapeptide NKIS. A linker could be inserted at the BamH1 site. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
                                                                                                                                                                                                                                                        a fragment of Group A streptococcal surface protein MS and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant hybrid streptococcal M protein antigen(s) - which elicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                          B subunit; labile toxin; M protein; fusion protein; antigen; Group A streptococci; rheumatic fever; pharyngitis.
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                                                                                                                                                                                                                                                                          carrier of the COOH-terminal portion of M5
                                                                                                                    AAR50228 standard; protein; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYTE-) UNIV TENNESSEE RES CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93WO-US008704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-00945860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASREAKKQVEKALE 118
                 ASREAKKQVEKALE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASREAKKQVEKALE 14
14
                                                                                                                                                                                                                        (first entry)
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1 ASREAKKQVEKALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mammalian heart tissue.
                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-118162/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
ses 14; Conserv
                                                                                                                                                                                                                                                                                                                                                            Streptococcus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ45160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 254 AA;
                                                                                                                                                                                  27-AUG-2003
25-MAR-2003
09-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                               WO9406465-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1994
                                                                                                                                                                                                                                                         Sequence of
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Dale JB;

opsonic

- useful

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Gaps

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(revised)

27-AUG-2003

AAR20128 standard; protein; 281 AA.

105

RESULT 12 AAR20128 ID AAR2

Query Match

Best Loc Matches

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antibody; heart tissue; antigen; serotype; mucosal.
                                                                                                                                                                                                                           31-MAR-1994.
                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB03117;
                                                                                                                                     Peptide
                                                                                    Peptide
                                                             Peptide
                                                                                                              Peptide
                                                                                                                                                               Peptide
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ID AABC
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AC AAB(
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     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                               The surface M protein of Group A streptococi is the major virulence factor and protective antigen of these organisms. However, there are a tremendous number of M protein servotypes. The invention provides recombinant M protein antigens comprising a gene encoding a carrier protein and an NH2 or COOH terminal M protein fragment carrying one or more epitopes. The carrier may be the B subunit of B.coli labile toxin (LT-B) or the C-repeat protion of a streptococcal M protein. Por example, AAQ45161/R50229 comprises three segments of MS designated A,B and C. The COOH-terminal half of MS. The carrier includes 2.5 C-repeats, which each commence with the tetrapeptide NKIS. A linker could be inserted at the BamH1 site. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                        New recombinant hybrid streptococcal M protein antigen(s) - which elicit opsonic antibodies without eliciting cross-reactive antibodies to mammalian heart tissue.
                                    Sequence of fragments of Group A streptococcal surface protein MS and a carrier of the COOH-terminal portion of MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer; PCR; amplify; polymerase chain reaction; construct; hybrid; M protein; M24; M5; M19; subunit; tetravalent protein; emm gene; tandem; pKK233; protective epitope; tissue-cross-reactive epitope; restriction enzyme site; multivalent M protein; immunisation; group A; streptococci; rheumatic fever; rheumatic heart disease; humoral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                        B subunit; labile toxin; M protein; fusion protein; antigen;
Group A streptococci; rheumatic fever; pharyngitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 64; DB 2; Length 284; 100.0%; Pred. No. 0.032; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant M24-M5-M6-M19 C-term variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR50996 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 5; 45pp; English.
                                                                                                                                                                                                                                      (UYTE-) UNIV TENNESSEE RES CORP.
                                                                                                                                                                                                             92US-00945860.
                                                                                                                                                                                      93WO-US008704
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              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
   (revised)
                                                                                                                                                                                                                                                                                       WPI; 1994-118162/14.
                                                                                                             Streptococcus sp.
                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ45161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 284 AA;
                                                                                                                                     WO9406465-A1
                                                                                                                                                                                                             16-SEP-1992;
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02-NOV-1994
25-MAR-2003
09-OCT-1994
                                                                                                                                                              31-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                              Dale JB;
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Matches
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The sequences given in AAR5092-1001 represent hybrid M proteins which contain the M24-M5-M6 and/or M19 subunits. These multivalent proteins were constructed using fragments of the 5' regions of emm genes that were amplified by PCR, ligated in tandem and expressed in pKK223.3. The amplified regions pref. encode protective and not tissue-cross-reactive epitopes, which can then be linked into one protein molecule. The recombinant hybrid protein may contain 113 N-terminal amino acids of M24, 58 amino acids specified by the respective restriction enzyme sites by 2 amino acids specified by the respective restriction enzyme sites Multivalent M proteins auch as this may be used for protective immunisation against group A streptococci, which esp. cause rheumatic fever and rheumatic heart disease. Humoral antibodies raised against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       these proteins do not react with heart tissue antigens but are effective against many different serotypes. The multivalent proteins may also include sequences which induce mucosal antibodies and do not require coupling to an immunogenic carrier. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunogenic hybrid proteins derives from streptococcal M proteins - induces opsonic antibodies, for protective immunisation against multiple group A streptococci serotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                             53. 69
/labol= M19
70. 305
/jabel= M5_C-terminal_fragment
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB03117 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYTE-) UNIV TENNESSEE RES CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93WO-US008703.
                                                                                                                                      36. .52
/label= M6
53. Fo
                                                       = M24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
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Best Local Similarity 100.
Marches 14; Conservative
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                                ..18
label:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-118122/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                          WO9406421-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1992;
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Job time : 79.7907 secs

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The invention relates to multivalent immunogenic hybrid group A streptococcal M proteins comprising N-terminal peptide fragments of M proteins comprising N-terminal peptide fragments of M proteins comprising N-terminal peptide fragments of G group A streptococci (e.g., Streptococca). The antibodies generated using the hybrid proteins are against one or more M protein generated using the hybrid proteins are against one or more M protein cerotypes, where at least one of the serotypes is MI, M3, MB or MB; The invention also encompasses a recombinant DNA molecule comprising a nucleotide sequence that encodes a multivalent hybrid M protein; and method for immunising a mammal against streptococcal infections, comprising an immunogenic multivalent hybrid M protein to the mammal. The multivalent hybrid M proteins are useful for eliciting opsonic or protective antibodies to the M proteins are useful for eliciting opsonic or protective antibodies to the M proteins are useful for eliciting opsonic or protective against and control infection by type A streptococci Type A streptococci are not only responsible for streptococcal pharyngitis (strep throat), forms of pneumonia and a condition resembling toxic shock, but are also involved in the development of acute rheumatic fever (ARF) and rheumatic hart disease. In a patient with ARF, antibodies formed during a group A streptococcal indicates that the streptococci and host tissue contain similar antigenic and many and a contain and a conservative with heart tissue, which indicates that the streptococci and host tissue contain similar antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       motifs. The new multivalent vaccines are capable of raising sero-specific antibodies against various serotypes of group A streptococci which are not cross-reactive with human heart tissue. Sequences AAB03113-B03117, AAB03119-B03121 and AAB03122 *** B03124 represent multivalent hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic recombinant hybrid M protein comprising amino-terminal peptide fragments of streptococcal M protein useful as vaccine against rheumatic fever and infections leading to rheumatic fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes M proteins generated in the disclosure of the
                                                                                       Multivalent hybrid M protein; group A streptococcus; serotype; immunogenic; sero-specific antibody; streptococcal infection; cross reactivity; vaccine; acute rheumatic fever; ARF; rheumatic chart disease; streptococcal pharyngitis; strep throat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 64; DB 3; Length 305; 100.0%; Pred. No. 0.034; tive 0; Mismatches 0; Indels
                                             S. pyogenes hybrid M protein (M24-M5-M6-M19), SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 8A-B; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYTE-) UNIV TENNESSEE RES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-00945954.
                                                                                                                                                                                                                                                                                                                                                                                                            97US-00937271
10-OCT-2000 (first entry)
                                                                                                                                                                                                                                         Streptococcus pyogenes.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dale JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-364475/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA57897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              LS-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lederer JW,
                                                                                                                                                                                                                                                                                                               US6063386-A
                                                                                                                                                                                                                                                                                                                                                              16-MAY-2000
                                                                                                                                                                                              pneumonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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ó 1 ASREAKKQVEKALE 14 Local Similarity 100. nes 14; Conservative

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Gaps

Search completed: August 4, 2005, 08:59:23

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Query Match 100.0%; Score 64; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 0.00068; Matches 14; Conservative 0; Mismatches 0; Indels
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acida
TYPE: amino acid
STRANDEDNESS:
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US-08-817-811-1
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Sequence 18, Appl
Sequence 17, Appl
Patent No. 5210183
Patent No. 5210183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                       August 4, 2005, 08:27:17; Search time 19.5349 Seconds (without alignments) 53.498 Million cell updates/sec
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Sequence 6, Ag
Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, P
Sequence 6, Al
Sequence 6, Al
Sequence 11,
Sequence 32,
Sequence 33,
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Sequence 83,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*

1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

6: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-914-479A-4

US-08-914-479A-6

US-08-917-271-10

US-08-312-276E-35

US-08-325-278B-6

US-08-817-811-34

US-08-817-811-31

US-08-817-811-32

US-08-817-811-33

US-08-817-811-33

US-08-817-811-33

US-08-817-811-33

US-08-817-811-33

US-08-817-811-33

US-08-817-811-30

US-08-817-811-30

US-08-817-811-30

US-08-817-811-10

US-08-817-811-10

US-08-817-811-10

US-08-817-811-10

US-08-817-811-10

US-08-817-811-10

US-08-817-811-16

US-08-817-811-16

US-08-817-811-16

US-08-817-811-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-464-531-83
US-08-461-598-83
US-08-322-137-83
US-08-307-896-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                            1 ASREAKKQVEKALE 14
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Maximum DB seq length: 200000000
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64
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Match Length
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                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
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No.
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Sequence 6, Appliance 6, Appliance 6, Appliance 61, Appliance 29, Appliance 29, Appliance 12, Appliance 12, Appliance 422, Appliance 422, Appliance 45471, Appliance 45471, Appliance 45471, Appliance 61, Appliance
                                                                                                                 1, APP--
12745, A
6, Appli
                                                                         Sequence
Sequence
Sequence
                                        Seguence
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US-08-817-811-1

US-08-817-811-1

Sequence 1, Application US/08817811

Fatent No. 6174528

GENERAL INFORMATION:

APPLICANT: Cooper, Juan A.

APPLICANT: Good, Michael F.

APPLICANT: Saul, Allan J.

TITLE OF INVENTION: COMPRISING SAME

NUMBER OF SEQUENCES: 97

TITLE OF INVENTION: COMPRISING SAME

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSE: ALNOIG, White & Durkee

STREET: Houston

STATE: Texas

CONPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER:
                         US-09-963-137-192
US-09-963-137-192
US-09-963-137-194
US-09-513-818-6
US-09-513-818-6
US-08-817-811-67
US-08-817-811-29
US-08-817-811-25
US-08-817-811-15
US-09-513-999-4696
US-09-513-999-4696
US-09-513-999-4696
US-09-513-999-4696
US-09-513-999-4696
US-09-513-999-4696
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, OTHER INFORMATION: An antigen of three fragments of MS and a carrier
, OTHER INFORMATION: of the COOH-terminal portion of MS
US-08-914-479A-6
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Patent No. 6419932

JERERAL INFORMATION:
APPLICANT: Dale, James B.
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
FILE REFERENCE: 481112.4 04C2
CURRENT APPLICATION NUMBER: US/08/914,479A

CURRENT APPLICATION NUMBER: 08/08/914,479A

PRIOR FILING DATE: 1995-03-23

PRIOR FILING DATE: 1995-09-16

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Fast-SEQ for Windows Version 4.0

LENGTH: 284
                                                                                                                                                                                           Query Match 100.0%; Score 64; DB 4; Length 254; Best Local Similarity 100.0%; Pred. No. 0.009; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 64; DB 4; Length 284; Best Local Similarity 100.0%; Pred. No. 0.01; Matches 14; Conservative 0; Mismatches 0; Indels
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; Patent No. 6063386
; GENERAL INFORMATION:
APPLICANT: Daile, James B.
TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                             FEATURE:
CTHER INFORMATION: An antigen of MS and a carrier of the
CTHER INFORMATION: COOH-terminal portion of MS
US-08-914-479A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 ASREAKKQVEKALE 148
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                  105 ASREAKKÖVEKALE 118
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COUNTRY: USA
ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-914-479A-6
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     LENGTH: 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                    Sequence 11, Application US/08937271
Patent No. 6063386
GENERAL INFORMATION:
APPLICANT: Dale, James B.
APPLICANT: Lederer, James W.
TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,271
FILING DATE: 15-SEP-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: Rosenman, Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 481112.405C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08914479A Patent No. 6419932 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-631
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 ASREAKKOVEKALE 100
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                              ASREAKKQVEKALE 20
1 ASREAKKQVEKALE 14
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: USA
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US-08-937-271-11
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Sequence 6, Application US/08325278B
Patent No. 6822075
GENERAL INFORMATION:
APPLICANT: Bjorck, Lars
Sjobring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 70.1 Fifth Avenue Suite 6300
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 64; DB 2; Length 443; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels
                           APPLICANT: Bjvrck, Lare
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278B
                                                                                                                                                                    STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: USA ZATE: Washington COUNTRY: USA ZIP: 98104-7092 COMPUTER READABLE FORM: WEDTON TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OFFRATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,475
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-FEB-1997
CLASSIFICATION: 435
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: MCMASters, David D.
REGIGSTRATION NUMBER: 33,963
REFRENCE/DOCKET NUMBER: 1000
TELECOMMUNICATION INFORMATION:
TELEPRAX: (206) 622-631
INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 443 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 443 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 ASREAKKOVEKALE 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-795-475-6
       GENERAL INFORMATION:
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Patent No. 6737521

GRERAL INPORMATION:
APPLICANT: POZZI, Gianni
APPLICANT: POZZI, Gianni
APPLICANT: SCHENTI, Vincent A.
APPLICANT: SCHENTION:
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
TITLE OF INVENTION NUMBER: US/08/302,756E
CURRENT APPLICATION NUMBER: US/07/42,199
PRIOR PILING DATE: 1990-05-11
PRIOR PELING DATE: 1991-12-23
PRIOR FILING DATE: 1991-12-23
PRIOR PILING DATE: 1991-12-23
PRIOR PILING DATE: 1991-12-3
PRIOR PILING DATE: 1991-03-12
PRIOR APPLICATION NUMBER: US/07/851,082
PRIOR APPLICATION NUMBER: PCT/US93/02355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 64; DB 3; Length 305; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                  481112.405C1
                              FILING DATE: 15-SEP-1997
CLASSIFICATION: 424
TORNEY/ACENT
                                                                 FILING DATE: L. C. C. CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROSENMAN, Stephen J. REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 48111
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-691
TELEPAX: (206) 682-691
SEQUENCE CHARACTERISTICS:
LENGTH: 305 anino acids
TYPE: minio acids
TYPE: minio acids
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Patent No. 5965390
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 14; Conservative
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; MOLECULE TYPE: protein
US-08-937-271-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: S. pyogenes
US-08-302-756E-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-302-756E-35
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RESULT 11
US-08-817-811-32
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Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WESULT 9
US-08-817-811-34

i Sequence 34, Application US/08817811

i Patent No. 6174528

i GENERAL INFORMATION:

APPLICANT: Cooper, Juan A.

APPLICANT: Relf, Wendy A.

APPLICANT: Good, Michael F.

APPLICANT: Sall, Allan J.

TITLE OF INVENTION: COMPRISING SAME

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 87.5%; Score 56; DB 3; Length 12; Best Local Similarity 100.0%; Pred. No. 0.0074; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IS PROPADIALE
COMPUTER: ENDORMY DISK
COMPUTER: IS PROPED COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: 424
PRICH APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REGISTRATION NUMBER: 37,642
REGISTRATION NUMBER: 37,642
REGISTRATION NUMBER: 31,642
RELEPHONE: 512/418-3000
TELEFPAN: 51
REFERENCE/DOCKET NUMBER: 100084.402
                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-325-278B-6
                          TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERRISTICS:
LENGTH: 443 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASREAKKQVEKALE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-817-811-34
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REBULT 10

Sequence 11, Application US/08817811

Sequence 11, Application US/08817811

Sequence 11, Application US/08817811

Parent No. 1614528

SEQUENCE 12, MINCHANION: To CAPATISING SAME

SEQUENCE SEQUENCES: To CAPATISING SAME

SEQUENCES: SAME SAME CONTRIBERS:

APPLICATION STATESTIC PEPTIDES AND VACCINES

ITITLE OF INVENTION: STATESTIC PEPTIDES AND VACCINES

ITITLE OF INVENTION: STATESTIC PEPTIDES AND VACCINES

TITLE OF INVENTION: STATESTIC PEPTIDES

APPLICATION STATESTIC PEPTIDES

CONTRIBERS READABLE FORM:

MEDIDIN TYPE: Tooks

CONTRIBER READABLE FORM:

MEDIDIN TYPE: TOOPP GIAN

CONTRIBER READABLE FORM:

MEDIDIN TYPE: TOOPP GIAN

CONTRIBER SEARCH CONTRIBER: DEPLECTION NATIONS STATESTIC PEPTIDES

CONTRIBER STATESTI
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3 REAKKQVEKALE 14

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Gaps
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US-08-817-811-18
is Sequence 18, Application US/08817811
is Patent No. 6174528
is Patent No. 6174528
is APPLICANT: Cooper, Juan A. APPLICANT: Cooper, Juan A. APPLICANT: Saul, Mendy A. APPLICANT: Saul, Allan J. TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES TITLE OF INVENTION: COMPRISING SAME NUMBER OF SEQUENCES: 97
is CORRESPONDENCES: 97
is CORRESPONDENCES: 97
is COUNTY: Houston
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.9%; Score 55; DB 3; Length 12; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.2%; Score 52; DB 3; Length 28; 78.6%; Pred. No. 0.075; tive 2; Mismatches 1; Indels
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                                                                                  FBRC: 005
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:
FELECOMMUNICATION INFORMATION:
FELEPHONE: 512/418-3000
FELEPHON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
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Best Local Similarity 78.6
Matches 11; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels
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Patent No. 6174528

GENERAL INFORMATION:

APPLICANT: Cooper, Juan A.

APPLICANT: Good, Michael F.

APPLICANT: Good, Michael F.

APPLICANT: Saul, Allan J.

TITLE OF INVENTION: COMPRISING SAME
TITLE OF INVENTION: UNITE & Durkee
STREET: P.O. BOX 4433

CITY: Houston
STREET: Texas

COUNTRY: USA

ZIP: TAXE
                                                                                                             COUNTRY: USA.

ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELEPHONE: 512/418-300
TELEPAX: 512/418-300
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CHARLATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
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BIDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
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   STREET: P.O. Box 4433
CITY: Houston
                                                                                      Texas
: USA
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                                                       Sequence 31, Application US/08817811
; Sequence 31, Application US/08817811
; Patent No. 617428
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYMTHETIC PEPTIDES AND VACCINES
; TITLE OF INVENTION: SYMTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Annold, White & Durkee
STREET: P.O. Box 4433
CITY: HOUSEON
COUNTRY: USA
ZIP: 77210
COMPUTER PT-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
CORPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: WO 96/11944
FRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELEFRAN: 512/418-3000
TELEFAX: 512/418-3000
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APPLICANT: Relf, Wendy A.
APPLICANT: Relf, Wendy A.
APPLICANT: Good, Michael F.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
TITLE OF INVENTION: COMPRISING SAME
VUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
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US-08-817-811-17
; Sequence 17, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
                                     10 ASREAKKQVEKKVK 23
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Best Local Similarity 100.
Matches 11; Conservative
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4, 2005, 08:38:31

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ADDRESSEE: Arnold, White & Durkee

CITY: Houston

STREET: D. Box 4433

CITY: Houston

STATE: Texas

CONFUTER: Lexas

CONFUTER: Dispy

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DoS/MS-DoS

SOFTWARE: Patenth Release #1.0, Version #1.30

CURFATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patenth Release #1.0, Version #1.30

CURFATION NUMBER: US/08/817,811

FILING DATE: 14-APR-1997

ATOMENT INFORMATION

NAME: Highland: Stark1996

ATOMENT INFORMATION:

NAME: Highland: Steven E-Stark

FELEPHONE: 37,642

REGISTRATION NUMBER: 937,642

REGISTRATION NUMBER: 937,642

REGISTRATION SEC IN NO: 17:

SEQUENCE CHARACTERISTICS:

LEMBORN: 512/418-3000

TELEPHONE: 212/418-3000

TELEPHONE: 212/418-3000

TELEPHONE: StarkACTREISTICS:

LENGTH: 28 amino acids

TOPOLOGY: linear

US-08-817-811-17

QUENT WARCH

BREEL LOCAL SIMILARITY 76.5%; Pred. NO. 0.38;

MATCHES 13; CONSERVATION 76.5%; Pred. NO. 0.38;

MATCHES 13; CONSERVATION 76.5%; Pred. NO. 0.38;

BREEL LOCAL SIMILARITY 76.5%; Pred. NO. 0.38;

MATCHES 13; CONSERVATORE 27

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Sequence 1, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 15, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 72, Appli
Sequence 1295, Appli
                                                                                                                             August 4, 2005, 08:36:38; Search time 68.3721 Seconds (without alignments) 79.939 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/US06_MW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_WW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_WW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USS0_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USS0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-044-034-22
US-10-706-275-5
US-10-706-275-2
US-10-706-275-15
US-10-11-627-4
US-10-141-627-6
US-08-325-278-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*
                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
Sequence:
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Maximum DB s
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                                                                                                                                 Run on:
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No.
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Sequence 13, Appl Sequence 14, Appl Sequence 11, Appl Sequence 10, Appl Sequence 5342, Ap Sequence 9, Appli Sequence 83, Appli	8 3 1 1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	100 100 100 100 100 100 100 100 100 100	Sequence 187, App Sequence 18, App1 Sequence 194, App Sequence 7889, Ap Sequence 7589, Ap Sequence 7620, Ap Sequence 7620, Ap
-275-1 -275-1 -275-1 -275-1 -275-9	-10-263-341-8 -10-600-003-8 -10-444-599-2 -10-732-923-7 -09-952-680A-10-408-765A-110-408-765A-110-7532-923-7	-09-952-680A-1 -10-215-982-16 -10-732-923-80 -10-732-923-80 -10-732-923-80 -10-732-923-80 -10-952-680 -09-953-131-19	US-10-116-275-187 US-10-352-843-18 US-10-315-982-13 US-10-684-422-194 US-10-732-923-7589 US-10-732-923-7592 US-10-732-923-7620 US-10-732-923-7620
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ALIGNMENTS

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APPLICANT: ID Biomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: Mitch of Gregory L.
APPLICANT: Good, Michael F.
APPLICANT: Batzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
ITIME OF INVENTION: Vaccine
FILE REFERENCE: 021989-000710US
CURRENT FILING DATE: 2003-11-13
RIOR APPLICATION NUMBER: US 60/426,409
PRIOR FILING DATE: 2002-11-15
RRIOR APPLICATION NUMBER: AU 2002302132
RRIOR APPLICATION NUMBER: AU 2002302132
RRIOR APPLICATION NUMBER: 2002-11-15
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: antigenic peptide sequence derivative of S. pyogenes US-10-706-275-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 64; DB 17; Length 1
100.0%; Pred. No. 0.0024;
:ive 0; Mismatches 0; Indels
Sequence 1, Application US/10706275
Publication No. US20050002956A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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US-10-474-792-672 US-10-732-923-3295 US-10-706-275-12

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RESULT 5
US-10-706-275-15
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APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, Goorge H.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: Good, Michael F.
APPLICANT: Barzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
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US-10-044-034-22
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                                                                                                                                                                                                                                 APPLICANT: O'BRIEN-STAFFON, DELL M.
APPLICANT: O'BRIEN-STAFFON, NEIL M.
APPLICANT: BRANDY, LORENA E.
APPLICANT: BEE, NICHOLAS J.
APPLICANT: BEADY, EVELYN R.
APPLICANT: GOOD, MICHAEL F.
TITLE OF INVENTION: POLYMERS: INCORPORTING PEPTIDES
FILE REFERENCE: FBRC.006
CURRENT FALING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: POSO71
PRIOR APPLICATION NUMBER: POSO71
PRIOR PILING DATE: 1997-02-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VET. 2.1
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; OTHER INFORMATION: antigenic peptide sequence p145
US-10-706-275-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: VOCATION TO THE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/426,409
PRIOR PELING DATE: 2002-11-15
PRIOR PELING DATE: 2002-11-15
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                    Sequence 22, Application US/10044034 Publication No. US20020169264A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/10706275 Publication No. US20050002956A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ASREAKKOVEKALE 14
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                                           1 ASREAKKÖVEKALE 14
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LENGTH: 20
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LENGIH: 20
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; OTHER INFORMATION: antigenic peptide derivative of S. pyogenes with flanking sequen; OTHER INFORMATION: eB
US-10-706-275-2
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                                                                                                                                                                                                                                                                                                              Sequence 2. Application US/10706275

Sequence 2. Application US/10706275

Publication No. US20050002956A1

GENERAL INFORMATION:
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: David S.
APPLICANT: Burt, David S.
APPLICANT: Good, Michael F.
APPLICANT: Good, Michael F.
APPLICANT: Good, Michael F.
APPLICANT: Good, Michael R.
APPLICANT: Bartzloff, Michael R.
APPLICANT: Bartzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
TITLE OF INVENTION: Vaccine
FILE REPREMENT: 2009-101-13
CURRENT APPLICATION NUMBER: US 60/426,409
PRIOR FILING DATE: 2002-11-15
PRIOR PILING DATE: 2002-11-15
PRIOR FILING DATE: 2002-11-15
PRIOR FILING DATE: 2002-11-15
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APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: Good, Michael F.
APPLICANT: Batzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
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      Length 20
                                                             0; Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 0;
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FILE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/426,409
PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: AU 2002302132
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 15, Application US/10706275; Publication No. US20050002956A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO
LENGTH: 29
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                                                                                                                       1 ASREAKKQVEKALE 14
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Gaps

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Sequence 672, Application US/10474792

Publication No. US20040236072A1

GENERAL INFORMATION:

APPLICANT: Olmsted, Stephen

APPLICANT: Mickarg, Elliot

APPLICANT: Wickarg, Elliot

TITLE OF INVENTION: SURECE PROTEINS OF STREPTOCCCCUS PYOGENES

FILE REFERENCE: AM 100399

CURRENT FILING DATE: 2003-10-14

NUMBER OF SEQ ID NOS: 674

SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM P. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278
FILLNG DATE: 26-OCT-1996
CLASSIFICATION: 435
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o
        Mismatches
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NAME: McMatters, David D.
REGISTRATION UNDER: 33,963
REFERENCE/DOCKET NUMBER: 450023.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-631
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 443 amino acids
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                                                                       294 ASREAKKÖVEKALE 307
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amino acid
                                               1 ASREAKKQVEKALE 14
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Best Local Similarity 100.
Matches 14; Conservative
      14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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LENGTH: 553
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                                                                                                                      OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: An antigen of three fragments of M5 and a carrier; OTHER INFORMATION: of the COOH-terminal portion of M5 US-10-141-627-6
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Sequence 6, Application US/10141627;
Publication No. US2020176863A1
GENERAL INFORMATION:
TATLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
TITLE OF INVENTION: POR GROUP A STREPTOCOCCAL VACCINE
TITLE OF INVENTION: POR GROUP A STREPTOCOCCAL VACCINE
CURRENT PRILICATION NUMBER: US/10/141,627
CURRENT FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 64; DB 13; Length 254; 100.0%; Pred. No. 0.049;
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                                                                                                                                                                                     Ouery Match 100.0%; Score 64; DB 17; Length 29; Best Local Similarity 100.0%; Pred. No. 0.0051; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10141627
Publication No. US20020176863A1
GENERAL INFORMATION:
APPLICANT DAIS, James B.
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
FILE REFERENCE: 481112.404C3
CURRENT APPLICATION NUMBER: US/10/141,627
CURRENT FILING DAIS: 2002-05-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 29
                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                 9 ASREAKKQVEKALE 22
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity
                                                                                                                                              US-10-706-275-15
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LENGTH: 254
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SEQ ID NO 13
LENGTH: 28
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Publication No. US20050002956A1
GENERAL INFORMATION
FRANCATION
FRAPLICANT: ID Bloomedical Corporation of Quebec
APPLICANT: Lowell, George H.
APPLICANT: David S.
APPLICANT: Burt, David S.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: Baraloff, Michael R.
APPLICANT: Leanderson, Tomas B.
TITLE OF INVENTION Vaccine
FILE REFERENCE: 021989-0007108
CURRENT FILING DATE: 2003-11-13
FRIOR APPLICATION NUMBER: US 60/426,409
FRIOR APPLICATION NUMBER: US 60/426,409
FRIOR APPLICATION NUMBER: AU 2002302132
FRIOR APPLICATION NUMBER: AU 2002302132
FRIOR PILING DATE: 2002-11-15
SUPPHARE: PALCH IN Version 3.1
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                                                                                                                                                                                                                                                                                                                                                         Sequence 3295, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TANGERIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15(52796)C

CURRENT APPLICATION NUMBER: US/10/712,923

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 3295
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                                                                                                  Query Match
100.0%; Score 64; DB 16; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 14; Conservative 0; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-672
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                                                                                                                                                                                                                                     404 ASREAKKQVEKALE 417
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1es 14; Conservative
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LENGIH: 28
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Sequence 14, Application US/10706275

Sequence 14, Application US/10706275

Publication No. US20050002956A1

GENERAL INFORMATION:
APPLICANT: ID Biomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Mitte, Gregory L.
APPLICANT: Batzloff, Michael F.
APPLICANT: Batzloff, Michael F.
APPLICANT: Batzloff, Wichael R.
APPLICANT: Batzloff, Wichael R.
APPLICANT: Batzloff, Wichael R.
TITE OF INVENTION: USCINE
FILE REFERENCE: 021989-000710US

CURRENT FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/426,409

PRIOR PAPLICATION NUMBER: US 60/266,409

PRIOR APPLICATION NUMBER: US 60/266,409

PRIOR PELING DATE: 2002-11-15

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIN version 3.1

SEQ ID NO 14

LENGTH: 28
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US-10-706-275-13
Sequence 13, Application US/10706275
Sequence 13, Application US/10706275
Publication No. US20050002956A1
GENERAL INPORMATION:
APPLICANT: ID Biomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: Mite, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: Hatzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
APPLICANT: Leanderson, Tomas B.
APPLICANT: Leanderson, Tomas C.
APPLICANT: Leanderson, Tomas C.
APPLICANT: Leanderson, Tomas C.
APPLICANT: Vaccinents
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                           Gaps
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US-10-706-275-13
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                           ö
Best Local Similarity 85.7%; Pred. No. 0.061; Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Vaccine
PILE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/426,409
PRIOR PLILNG DATE: 2002-11-15
PRIOR PLILNG DATE: 2002-11-15
PRIOR PLILNG DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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                                                                                      1 ASREAKKQVEKALE 14
                                                                                                                                              9 ASREAKKÖVEKAVK 22
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APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: Burt, David S.
APPLICANT: Burt, Geogy L.
APPLICANT: Burt, Michael R.
APPLICANT: Batzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: 021989-0007100S
CURRENT FILING DATE: 2003-11-13
FRIOR APPLICATION NUMBER: US 60/426,409
FRIOR PELING DATE: 2002-11-15
FRIOR PELING DATE: 2002-11-15
FRIOR PELING DATE: 2002-11-15
FRIOR FILING DATE: 2002-11-15
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Publication No. US20050002956A1

GENERAL INFORMATION:

APPLICANT: ID Biomedical Corporation of Quebec

APPLICANT: Lowell, George H.

APPLICANT: Lowell, George H.

APPLICANT: White, Gregory L.

APPLICANT: Burt, David S.

APPLICANT: Michael F.

APPLICANT: Batzloff, Michael R.

APPLICANT: Batzloff, Michael R.

APPLICANT: Leanderson, Tomas B.

TITLE OF INVENTION: Vaccine

FILE REFERENCE: 021989-000710US

CURRENT APPLICATION NUMBER: US/10/706,275

CURRENT FILING DATE: 2003-11-13

FRIOR APPLICATION NUMBER: US 60/426,409
                                                               FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-14
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87.5%; Score 56; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/10706275
Publication No. US20050002956A1
GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 28
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

August 4, 2005, 08:50:19; Search time 15.3023 Seconds (without alignments) 88.028 Million cell updates/sec

1 ASREAKKQVEKALE 14 US-10-706-275-1 64 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	rip	plasminogen-bindin	protein M precurso	M protein precurso	plasminogen-bindin	plasminogen-bindin	M6 protein - Strep	ď		M1.1 protein precu	M5 protein precure	Ω	IgG-binding protei		in	M protein precurso			conserved hypothet	hypothetical prote	conserved hypothet	M protein-like mol	Fc-binding protein	M-like protein emm	IgA receptor precu	M protein precurso	M49 protein precur	IgA receptor - Str	. M2 protein precurs	. GTP-binding regula
SUMMARIES		A49545	S30283	530284	S43556	S43554	A26297	835401	S46489	S34978 ·	A28616	A44643	S57835	S54871	A28549	A60115	JC1419	T32382	C81248	T48000	H64327	PH0139	B54128	S49550	805568	S54858	A43715	S37046	S23325	A46685
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	ngt	388	408	436	454	472	483	484	484	484	492	501	528	532	539	564	587	546	149	423	104	168	365	384	386	386	389	402	407	91
di		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	70.3	68.8	68.8	67.2	•			•	67.2		•	67.2	9.59
	Score	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	45	44	44	43	43	43	43	43	43	43	43	43	42
	Result No.	-	7	m	4	S	9	7	80	Q	10	11	12	13	14	15	16	17		19	20	21	22	23	24	25	56	27	28	29

GTP-binding regula	hypothetical prote	H+-transporting tw	hypothetical prote	hypothetical prote	ribosomal protein	small protein B BH	emm L 15 protein -								
RGMSA1	RGHUA1	RGHYAE	RGMSA2	RGHYA2	RGRTA2	533458	RGHUA2	RGPGA2	T22180	T06930	A86641	T23007	S78352	H84093	S52537
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377	380	394	394	394	394	394	395	397	493	132	269	1328	127	157	377
65.6	9.59	9.59	9.59	9.59	65.6	9.59	65.6	9.59	9.59	64.1	64.1	64.1	62.5	62.5	62.5
42	42	42	42	42	42	42	42	42	42	41	41	41	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

plasminogen-binding protein PAM precursor - Streptococcus pyogenee (fragment)
N;Alternate names: plasminogen-binding M-like protein (Pd 53)
C;Species: Streptococcus pyogenee
C;Species: Streptococcus pyogenee
C;Accession: A49545; S61084; S60829; S70459; S32619
R;Berge, A.; Sjoebring, U.
B;Berge, A.; Sjoebring, U.
A;Title: PAM, a novel plasminogen-binding protein from Streptococcus pyogenee.
A;Reference numbor: A49545; MUID:94064605; PMID:8244975

A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-388 <-BER.
A; Residues: 1-388 <-BER.
A; Cross-references: UNIPROT: P49054; EMBL: Z22219; NID: 9288978; PIDN: CAA80222.1; PID: 9940
R; Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
B; Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
A; Whatmore, BMBL Data Library, July 1994
A; Description: Noncongruent relationships between variation in emml gene sequences and
A; Reference number: S61072

A;Accession: S61084

A; Molecule type: DNA
A; Residues: 13-96 < WHA.
A; Residues: 13-96 < WHA.
A; Residues: 13-96 < WHA.
A; Cross=references: EMBL: U11975; NID: 9533627; PIDN: AAA99591.1; PID: 91235829
A; Experimental source: serotype M53
B; Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A; Title: Non-congruent relationships between variation in emm gene sequences and the po
A; Reference number: S60784; MUID: 95198537; PMID: 7891551
A; Accession: S60829

A;Accession; Sougez's
A;Accession; Sougez's
A;Accession; Sougez's
A;Accession; Sougez's
A;Residues: 17-7 < KWHW.
A;Residues: 17-7 < KWHW.
A;Cross-references: EMBL:U11975
A;Experimental source: serotype M53
A;Experimental source: serotype M53
A;Experimental source: serotype M53
A;Experimental source: serotype M53
A;Accession: Stock-578, 1995
A;Accession: Stock-578, 1995
A;Accession: Stock-578, MUD:96342385; PMID:8748039
A;Reference number: S70459
A;Reference number: S70459
A;Reference number: S70459
A;Residues: 30-162 < CAR-54
A;

Gape ö ch 100.0%; Score 64; DB 2; Length 388; I Similarity 100.0%; Pred. No. 0.019; 14; Conservative 0; Mismatches 0; Indels Query Match Best Local S: Matches 14

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1 ASREAKKOVEKALE 14

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Gaps

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plasminogen-binding protein MLC36 - Streptococcus sp. (fragment)
C;Species: Streptococcus sp.
C;Species: Streptococcus sp.
C;Accession: S45598; S43556
R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebring, U.
Bur, J. Blochem. 222, 267-276, 1994
A;Title: Streptokinase activates plasminogen bound to human group C and G streptococci A;Reference number: S45598; MUID: 94291620; PMID: 8020466
A;Reference number: S45598; MUID: 94291620; PMID: 8020466
A;Reference number: S45598
A;Reference number: S45598
A;Reference number: S45598
A;Reference number: S45598
A;Residue: preliminary
A;Molecule type: DNA
A;Residues: 1-454 cBE2>
A;Residues: 1-454 cBE2>
A;Cosserreferences: EMBL: Z32677; NID: 9474767; PIDN: CAAB3588.1; PID: 9474768
C;Superfamily: M5 protein
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M6 protein - Streptococcus pyogenes

C;Species Streptococcus pyogenes

C;Species: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004

C;Accession: A26297

K;Hollingshead, S.K.; Fischetti, V.A.; Scott, J.R.

J. Biol. Chem. 261, 1677-1686, 1986

A;Title: Complete nucleotide sequence of type 6 M protein of the group A streptococcus.

A;Reference number: A26297; MUID:86111835; PMID:3511046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   System in the control of the control
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                                            Length 436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        match 100.0%; Score 64; DB 2; Local Similarity 100.0%; Pred. No. 0.022; es 14; Conservative 0; Miamatchee A
                                                 100.0%; Score 64; DB 2; 100.0%; Pred. No. 0.022;
                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                     332 ASREAKKOVEKALE 345
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                                                                                                                                                                                                                                                   1 ASREAKKQVEKALE 14
         Query Match
Best Local Similarity 100.v
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R; Podbielski, A.
Mol. Gen. Genet: 237, 287-300, 1993
A; Title: Three different types of organization of the vir regulon in group A streptococc
A; Reference number: $30283; MUID:93204905; PMID:8455563
A; Accession: $30283
A; Molecule type: DNA
A; Residues: 1-408 around acquence not shown
A; Residues: 1-408 around acquencing of group A streptococcal emm41/52 (ev
A; Description: Por mediated cloning and sequencing of group A streptococcal emm41/52 (ev
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-230, NV, 232-371, RV, 373-408 around acquencing
C; Genetics:
A; Cross-references: EMBL:X58178; NID:947362; PIDN:CAA41167.1; PID:947363
C; Genetics:
A; Genetics:
A; Cross-reference emm
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Albeaription: Por mediated cloning and sequencing of group A streptococcal emm41/52 (ev A). Reference number: $29680
A).Reference number: $29680
A).Reference number: $29680
A).Residues: 1-216, Val. 218-436 ePOD2>
A).Residues: 1-216, Val. 218-436 ePOD2>
A).Cross-references: EMBL:X58179; NID:g47364; PIDN:CAA41168.1; PID:g47365
C).Genetics:
A).Genetics:
C).Superfamily: M5 protein
C).Superfamily: M6 protein #status predicted <NAT>
C).Superfamily: M7 protein #status predicted <NAT>
C).Superfamily: M5 protein #status predicted <NAT>
C).Superfamily: M5 protein #status predicted <NAT>
C).Superfamily: M5 protein #status predicted <NAT>
C).Superfamily: M6 protein #status predicted <NAT>
C).Superfamily: M7 protein #status predicted <NAT>
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C).Superfam
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                                                                                                                                                                                                                                                   protein M precursor - Streptococcus pyogenes (serotype M41)
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C;Keywords: tranamembrane protein
C;Keywords: tranamembrane protein
F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-408/Product: M protein #status predicted <MAT>
F;383-401/Domain: transmembrane #status predicted <TMM>
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    266 ASREAKKQVEKALE
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M.1 protein precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: 334978; 531966
R;Harbaugh, M.P.; Podbielski, A.; Huegl, S.; Cleary, P.P.
Mol. Microbiol. 8, 981-991, 1993
Mol. Microbiol. 8, 981-991, 1993
A;Title: Nucleotide subbtitutions and small-scale insertion produce size and antigenic A;Reference number: 334978; MulD:93360826; PMID:8355619
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-484 <HAR>A;Residues: 1-484 <HAR>A;Residues: UNIPROT:Q05464; EMBL:Z21845; NID:g49401; PIDN:CAA79893.1; PID:g4940
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M5 protein precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
A;Variety: serctype ascretype
C;Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
C;Accession: A28616; S60787
E;Miller, L.; Gray, L.; Beachey, E.; Kehoe, M.
J Biol. Chem. 263, 5668-5673, 1988
A;Title: Antigenic variation among group A streptococcal M proteins. Nucleotide sequenc
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A;Residues: 1-492 «MIL»
A;Cross-references: UNIPROT:P02977; GB:M20374; NID:g153812; PIDN:AAA26976.1; PID:g15381
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
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A Molecule type: DNA
A Residues: 1-484 < AKES.
A, Residues: 1-484 < AKES.
A, Cross-references: UNIPROT:Q05464; UNIPROT:Q10372; UNIPROT:Q99XVO
A, Experimental source: strain 40/58, serotype M1
A, Accession: S46490
A, Molecule type: protein
A, Residues: 42-51 < AKW>
A, Experimental source: strain 40/58, serotype M1
C, Genetics:
A, Gene: emml
C, Superfamily: M5 protein
C, Keywords: transmembrane protein
C, Keywords: transmembrane protein
F;1-41/Domain: signal sequence #status predicted <SIG>F;42-484/Product: M1 protein #status experimental <MAT>F;459-477/Domain: transmembrane #status predicted <TWM>
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C;Keywords: membrane protein
P;1-42/Domain: signal sequence #status predicted <SIG>P;43-484/Product: M1.1 protein #status predicted <MAT>
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Cispecies: Streptococcus pyogenes
Cispecies: Streptococcus pyogenes
Cispecies: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
CiAccession: 846489; 846490
RiAkesson, P.; Schmidt, K.H.; Cooney, J.; Bjoerck, L.
Biochem. J. 300, 877-886, 1994
A;Title: MI protein and protein H: IgGFc- and albumin-binding streptococcal surface prob
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R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pog A;Reference number: S60784; MUID:95198537; PMID:7891551
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A; Molecule type: DNA
A; Residues: 1-484 <PDD>
A; Residues: 1-484 <PDD>
A; Cross-references: UNIPROT: Q10372; EMBL: X62131; NID: 9311757; PIDN: CAA44062.1; PID: 93117
B; Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
B; Whatmore to the EMBL Data Library, July 1994
A; Description: Noncongruent relationships between variation in emml gene sequences and the A; Reference number: S61072
A;Molecule type: DNA
A;Residues: 1-483 <HOL>
A;Residues: 1-483 <HOL>
A;Cross-references: UNIPROT:P08089; GB:M11318; GB:M11415; NID:g153699; PIDN:AAA26920.1;
C;Genetics:
A;Gene: emm6
C;Superfamily: M5 protein
C;Keywords: coiled coil; transmembrane protein
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C;Species: Streptococcus pyogenes
A;Variety: serotype MI
C;Date: 31-Dec.1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S35401; S61074; S60784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, September 1991
A;Reference number: S35401
A;Accession: S35401
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Best Local Similarity 100.8
Matches 14; Conservative
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A; Residues: 16-94 < WHA>
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A; Residues: 29-89 <WH2>
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62, 1336-1347, 1994
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C.Species: Streptococcus pyogenes
C.Species: Streptococcus pyogenes
A.Variety: serotype MS7
C.Species: Streptococcus pyogenes
A.Variety: serotype MS7
C.Species: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C.Accession: A44643; $60833
R.Maniluia, B.N.; Khandke, K.N.; Pairwell, T.; Relf, W.A.; Sriprakash, K.S.
J. Protein Chem. 10, 369-384, 1991
A.Fille: Hepted motifs within the distal subdomain of the coiled-coil rod region of A; Reference number: A44643; MUID:92143933; PMID:1781883
A.Feference of the MS7 serain A995
A.Ference extracted from NCBI backbone (NCBIN:8377, NCBIP:83738)
A.Ference of this sequence were confirmed by peptide sequences and the pop A.Ference number: 860934; MUID:95198377; PMID:7991521
A.Accession: 856033
A.Ference number: 860784; MUID:95198377; PMID:7991521
A.Accession: 856033
A.Ference number: 860784; MUID:95198377; PMID:7991531
A.Ference number: 860784; MUID:95198377; PMID:799154
A.Ference number: 860934; MUID:9519847; MUID:9519847; MUID:9519847; MUID:95
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N/Alternate names: IgG-binding protein type IIa; type IIa immunoglobulin G-binding prote
C/Species: Streptococcus pyogenes
A;Variety: strain 64/14
C;Date: 28-Nov-1995 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C;Accession: S57835; S58931
R;Boyle, M.D.P.; Hawlitzky, J.; Raeder, R.; Podbielski, A.
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A,Title: Non-congruent relationships between variation in emm gene sequences and the p. A;Reference number: $60784; MUID:95198537; PMID:7891551
A;Accession: $60784; MUID:95198537; PMID:789754343434
A;Accession: $60784; MUID:95198537; PMID:789754
A;Accession: $60784; MUID:95198537; PMID:789754
A;Accession: $60784; PMID:789754
A;Acc
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Best Local Similarity 100.(
Matches 14; Conservative
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A,Title: Analysis of genes encoding two unique type IIa immunoglobulin G-binding protein A;Reference number: S57834; MUID:94178942; PMID:8132341
A;Recession: S57835
A;Rocession: S57835
A;Roclecule type: DMD
A;Residues: 1-528 < ADO:
A;Cross-references: UNIPROT:Q54843; EMBL:X72932
A;Cross-references: UNIPROT:Q54843; EMBL:Q54843; EMBL:X72932
A;Cross-references: UNIPROT:Q54843; EMBL:Q54843; EMBL:Q54843; EMBL:Q54843; EMBL:Q54843; EMBL:Q54843; EMBL:Q54843; EMBL:Q5
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F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-528/Product: type IIa immunoglobulin G-binding protein emml #status predicted <MAT>
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S54871
M protein - Streptococcus sp.
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
E;PodbielBki, A.; Melzer, B.
B;PodbielBki, A.; Melzer, B.
B;PodbielBki, A.; Melzer, B.
B;PodbielBki, B;PodbielBki
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A;Variety: serotype M24
A;Variety: serotype M24
A;Variety: serotype M24
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A28549; 860802
R;Mouw, A.R.; Beachey, E.H.; Burdett, V.
J. Bacteriol. 170, 676-684, 1988
A;Title: Molecular evolution of streptococcal M protein: cloning and nucleotide sequence A;Reference number: A28549; MUID:88115166; PMID:3276665
A;Accession: A28549
A;Molecular type: DNA
A;Molecular type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-539 < MOUD
A;Cross-references: UNIPROT:P12379; GB:M19031; NID:g153616; PIDN:AAA26874.1; PID:g153617
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
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A;Accession: SS8931
A;Molecule type: DNA
A;Residues: 1-46, E', 48-52, E', 54-528 <POD>
A;Cross-references: EMBL:X72932; NID:9507128; PIDN:CAA51437.1; PID:9507130
C;Genetics:
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M24 protein precursor - Streptococcus pyogenes
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1 ASREAKKQVEKALE 14
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Job time : 16.3023 secs
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A; Mesidues: 42-54 < KRAP.
R; R; Chen., C.; Bormann, N.; Cleary, P.P.
Mol. Gen. Genet. 241, 685-693, 1993
Mol. Gen. Genet. 241, 685-693, 1993
A; Title: VirR and Mry are homologous trans-acting regulators of M protein and CSa peptid
A; Mcference number: $39886; MUID:94088463; PMID:7505389
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A; Residues: 13-111 cWHA>
A; Residues: 13-111 cWHA>
A; Cross-references: ENBL:U11937; NID:9533551; PIDN:AAA99553.1; PID:91235807
A; Cross-references: ENBL:U11937; NID:953351; Musser, J.M.; Kehoe, M.A.
B; Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
B; Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
A; Title: Non-congruent relationships between variation in emm gene sequences and the pop
                                                         A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60802
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 30-098 < WHA>
C;Superfamily: MS protein
C;Keywords: coiled coil; transmembrane protein
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R;Kraus, W.; Seyer, J.M.; Beachey, E.H.
Riffect. Immun. 57, 2457-2461, 1989
A;Title: Vimentin-cross-reactive epitope of type 12 streptococcal M protein.
A;Reference number: A60115; MUID:89307564; PMID:2473037
A;Accession: A60115
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A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
B, Molecule type: DNA
B, Molecule type: DNA
B, Molecule type: M.
B, Molecule type: Molecule to the Board type: M.
B, Molecule type: Molecule to the Board type: Molecule ty
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A;Variety: serotype M12
A;Variety: serotype M12
C;Date: O8-Dec-1992 #sequence revision O8-Dec-1992 #text_change O9-Jul-2004
C;Accession: A40174; A60115; $39887; $61072; $60793
R;Robbins, U.C.; Spanier, U.G.; Jones, S.J.; Simpson, W.J.; Cleary, P.P.
J. Bacteriol. 169; $633-5640, 1987
A;Title: Streptococcus pyogenes type 12 M protein gene regulation by upstres
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Pred. No. 0.026;
; Mismatches 0; Indels
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F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-564/Product: M protein (fragment) #status predicted <MAT>
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Mol. Microbiol. 14, 619-631, 1994
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Best Local Similarity 100.
Matches 14; Conservative
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A; Residues: 1-564 <ROB>
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Query Match
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MEDLINE=95172752; PubMed=7868273;
Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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MEDLINE=95172752; PubMed=7868273;

Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;

Musser J.M., Kapur V. azeto J., Pan X., Swanson D.S., Martin D.R.;

"Genetic diversity an relationships among Streptococcus pyogenes
strains expressing serotype MI protein: recent intercontinental spread
of a subclone causing episodes of invasive disease.";

Infect. Immun. 63:994-1003(1995).

EMBL; U20102; AAA85115.1; --

EMBL; U20101; AAA85118.1; --

EMBL; U20101; AAA85118.1; --

HSSP; P13276; 1EQ1.
"Genetic diversity and relationships among Streptococcus pyogenes strains expressing serotype M1 protein: recent intercontinental spread of a subclone causing episodes of invasive disease."; Infect. Immun. 63:994-1003 (1995). EMBL; U20104; AAA85117.1; -. HSSP; P13276; 1EQ1.
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
Streptococcus.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                        100 AA; 11287 MW; 9773331914EDC2D3 CRC64;
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100 AA; 11345 MW; 9773331C00EDC2D3 CRC64;
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
M1 protein (Fragment).
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InterPro; IPR003345; M_repeat.
                                                                                                                                                                        GO; GO: 0016020; C: membrane; IEA.
InterPro; IPR003345; M repeat.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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NCBI_TaxID=1314;
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SEQUENCE
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SEQUENCE
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CSTRAIN=3-3/317,
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MEDLINE=93062420; PubMed=1435517;
Podbielski A., Baird R., Kaufhold A.;
"The group A streptococcal M-type 3 protein gene exhibits a C terminus
typical for class I M proteins.";
Med. Microbiol. Immunol. 181:209-213(1992).
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Brandt E.R., Good M.F.;
Submitted (Hog-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
EMBL, UGS999; AB40640.1; -.
GO; GO:0009986; C:cell surface; IEA.
GO; GO:0005618; C:cell surface; IEA.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF00746; Gram_pos_anchor; 1.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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TIGRFAMB; TIGR01167; LPXTG_anchor; 1.
PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
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                                                                                                                                                                                                                                                                                                                                                   0, Indels
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AY225412; AA067526.1; -.
GO, 50016000; C:membrane; IEA.
InterPro; IPR000345; M_repeat.
Pfam; PF02370; M; 2.
NON_TER 1
CHAIN 2.3 >212 M protein.
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Bacteria, Firmicutes, Lactobacillales, Streptococcacese, Streptococcus, MCBI_TaxID=1314;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
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NON TER 212 212
SEQUENCE 212 AA; 24116 MW; 0A7EB56F0FCAEF26 CRC64;
                                                                                                                                                                                                                                                                       208 AA; 22565 MW; 79972A987324729B CRC64;
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Last annotation update)
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Last annotation update)
             EMBL, U66005; ABB46642.1; -...
GO; GO:000986; C:cell surface; IEA.
GO; GO:001620; C:cell surface; IEA.
GO; GO:001620; C:membrane; IEA.
InterPro; IPR001899; Gram_Dos_anchor.
InterPro; IPR001899; Gram_Dos_anchor.
Pfam; PF00746; Gram_Dos_anchor.
Pfam; PF00746; Gram_Dos_anchor; I.
PRMITS; PR0016; GPSOANCHOR.
TIGREAMS; TIGGO1167; LPXTG anchor; I.
PROSITE; PSSO847; GRAM_POS_ANCHORING; I.
CCell wall; Peptidoglycan-anchor.
NON TER
100 208
SEQUENCE 208 AA; 22565 WW; 79972A98732.
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   an amide bond (By similarity).
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QGTLR5;
05-JUL-2004 (TEMBLEEL: 27,
05-JUL-2004 (TEMBLEEL: 27,
05-JUL-2004 (TEMBLEEL: 27,
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 100.0
Matches 14; Conservative
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Best Local Similarity
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Name=emm;
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Name=emm;
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A Brandt ER., Good M.F.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

- I- SUBCELLUIAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).

EMBL; U65900; ABA840641.1; --

GO; GO:0005986; C:cell surfece; IEA.

GO; GO:0005618; C:cell wall; IEA.

GO; GO:0016020; C:membrane; IEA.

R InterPro; IPR0013945; M repeat.

R InterPro; IPR0013945; M repeat.

R Pfam; PF00776; Gram_pos_anchor, 1.

R Pfam; PF00776; Gram_pos_anchor; 1.

R Pfam; PF00776; Gram_pos_anchor; 1.

R Pfam; PF00776; M; L.

TIGRPAMS; TIGR01167; LPXTG_anchor; 1.

R PROSITE; PS60847; GRAM POS_ANCHORING; 1.

M PROSITE; PS60847; GRAM POS_ANCHORING; 1.
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Brandt E.R., Good M.F.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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                                 Query Match 100.0%; Score 64; DB 2; Length 208; Best Local Similarity 100.0%; Pred. No. 0.082; Matches 14; Conservative 0; Mismatches 0; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;
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                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAX-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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RESULT 10

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                                                                     Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A., McMillan D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A., McMillan D.;
                                                                                                                                                                                                                                                  100.0%; Score 64; DB 2; Length 279; 100.0%; Pred. No. 0.11; cive 0; Mismatches 0; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                        Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY139420; AANG4693.1; -. G.; GO:0016020; C.membrane; IEA. InterPro; IRR003345; M_repeat. PF02370; M; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY139401; AAN64674.1; -. G.; GO:0016020; C:membrane; IEA. InterPro; IRR003345; M_repeat. PF02370; M; 1.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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279 AA; 31224 MW; 16A600455BC5C3A0 CRC64;
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Last annotation update)
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Name=emm;
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NCBI_TaxID=1314;
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                                                     MEDLINE-22894607; Pubmed=14532198;

MOSES A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shetzigovsky I., Ravins M., Kozenman Z., Cohen-Poradosu R., Nir-Paz R.;

Ravins M., Kozenman Z., Cohen-Poradosu R., Nir-Paz R.;

"emm typing of M nontypeable invasive group A streptococcal isolates in Israel.";

J. Clin. Microbiol. 41:4655-4659(2003).

BMBL; AY394538; AAQ94530.1;

GO; GO:0016020; C:membrane: IEA.

InterPro; IPR003345; M_repeat.

Pfam; PP02370; M; 1.
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STRAIN-JS8;
Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shtzigovsky I.,
Ravins M., Korenman Z., Cohen-Poradosu R., Nir-Paz R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY346386; AAQ73206.1;
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR003345; M_repeat.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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251 AA; 28938 MW; 2A66602AAA637D11 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
M protein (Fragment).
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01-MAR-2004 (TrEMBLrel. 26, Last anno
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Matches 14; Conservative
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Name=emm;
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NCBI_TaxID=1314;
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        Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A., McMillan D., McMillan D., Submitted (Aug-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (Aug-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY13409; AAN64682.1; -.

GO; GO:0016020; C:membrane; IEA.

InterPro; IPR001345; M_repeat.

Pfam; PF02370; M; 2.

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SEQUENCE 303 AA; 34562 MW; F76F37540E16CD1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Dylar S., Sriprakash K.S., Delvecchio A., Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A., Smchillan D.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
                                                                                                                                                                       Ouery Match 100.0%; Score 64; DB 2; Length 303; Best Local Similarity 100.0%; Pred. No. 0.12; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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307 AA; 34955 MW; 2268229938E66E0E CRC64;
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GO; GO:0016020; C:membrane; IEA.
InterPro; IPR003345; M_repeat.
Pfam; PP02370; M; 2.
NON TER 307 307
SEQUENCE 307 AA; 34955 MW; 226
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NCBI_TaxID=1314;
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NCBI_TaxID=1314;
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Adb03117 S. pyogen Adp49327 S. pyrogen Aar97453 Chimaeric Abu39221 Protein e Adl99394 Manostruc Aar97499 Chimaeric Aar97390 Streptoco Aar97490 Streptoco Aar97460 Chimaeric Aar37701 SSP-8eg34 Adf60105 Synthetic Aar37765 SSP-8e3742 Chimaeric Aar37765 SSP-8e374 Adf60105 Synthetic Aar37765 SSP-534 p Aar37765 SSP-534 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention realtes to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid sequence of T helper cell epitope and B cell epitope, where amino acid sequences are different, and internal lysine residues or internal lysine analog residues for covalent attachment of each of lipid moieties through acepr; amino group or terminal side chain group of lysine or lysine analog. The peptides are useful in eliciting the production of antibody against an antigenic B cell epitope in a subject, and are useful for antibody production, synthetic vaccine production, diagnostic method employing antibodies and antibody ligands and immunotherapy for veterinary and human medicine. The method efficiently elicits the production of antibody against antigenic B cell epitope. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel lipopeptide comprising polypeptide having amino acid sequence of helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T helper cell epitope, B cell epitope, Antibacterial, Antiulcer, Antinfertility, Vaccine, antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic lipopeptide of the invention #101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES
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                                             AAR97439
ABU39221
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   WPI; 2004-238735/22.
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   Adk00565 Immunogen
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Adk00570 Immunogen
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Aaw04355 Chimaeric
Aaw04357 Chimaeric
Aaw10221 Streptoco
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Aar1020 Streptoco
Aar303015 Streptoco
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Abp30015 Streptoco
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17 KQAEDKVKASREAKKQVEKALEQLEDKVK 45
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                                                                                                                                                                                                   Synthetic.
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                                                                                       ADK00569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen.
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sequence represents a novel immunogenic lipopeptide comprising {\tt T} helper and {\tt B} cell epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel lipopeptide comprising polypeptide having amino acid sequence of helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus
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100.0%; Pred. No. 1.8e-09;
tive 0; Mismatches 0;
                                                             Score 137; DB 8;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                        Immunogenic lipopeptide of the invention #107.
                                                   100.0%; Scc... 100.0%; Pred. No. 1... 0; Mismatches
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                                                                                                              1 KOAEDKVKASREAKKQVEKALEQLEDKVK 29
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                                                                                                                                                                                                ADK00571 standard; peptide; 45 AA
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                                                         Query Match
Best Local Similarity 100.
Matches 29; Conservative
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and B cell epitopes
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                                   Sequence 29 AA;
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                                                                                                                                                                                                                                                                                                                                     Synthetic.
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The present invention realtes to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid sequence of T helper cell epicope, where amino acid sequences are different, and internal lysine residues or internal lysine analog residues for covalent attachment of each of lipid moieties through tegr; amino group or terminal side chain group of lysine or lysine analog. The peptides are useful in eliciting the production of antibody against an antigenic B cell epitope in a subject, and are useful for antibody production, synthetic vaccine production, diagnostic method employing antibodies and antibody ligands and immunotherapy for oveterinary and human medicine. The method efficiently elicites the production of antibody against antigenic B cell epitope. The present sequence represents a novel immunogenic lipopeptide comprising T helper and B cell epitopes.
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100.0%; Pred. No. 1.9e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                               Immunogenic lipopeptide of the invention #105.
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ADK00569 standard; peptide; 46 AA
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The present invention realtes to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid sequence of T habber cell epitope and B call epitope, where amino acid sequences are different, and internal lyshme residues or internal lyshme analog residues for covalent attachment of each of lipid moieties through kegr; amino group or terminal side chain group of lyshme or lyshme analog. The peptides are useful in eliciting the production of antibody against an antigenic B cell epitope, in a subject, and are useful for antibody production, synthetic vaccine production, diagnostic method employing antibodies and antibody ligands and immunotherapy for veterinary and human medicine. The method efficiently ellcits the production of antibody against antigenic B cell epitope. The present sequence represents a novel immunogenic lipopeptide comprising T helper
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                                                                                                                                                                                                                          Novel lipopeptide comprising polypeptide having amino acid sequence of helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus
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/note= "p145 conformational B-cell epitope"
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100.0%; Pred. No. 1.9e-09;
iive 0; Mismatches 0;
                                                                                           (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES
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                                                                                                                                                                                                                                                                                                                                             Claim 39; SEQ ID NO 106; 194pp; English.
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    12-AUG-2003; 2003WO-AU001018
                                                 12-AUG-2002; 2002US-0402838P.
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Matches 29; Conservative
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Immunogenic lipopeptide of the invention #108
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     Jackson D,
                                                                                                              Synthetic.
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RESULT 5

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Length 47;

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Cooper JA, Relf WA,
                                                                        WPI; 1996-221939/22
  (HALL-) HALL INST
(BIOT-) BIOTECH ?
(CSLC-) CSL LTD.
                                                                                                                                                                                                                                                                                                                                          Sequence 28 AA;
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(CSIR)
(UYME)
(HALL-)
(BIOT-)
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                                                                                                                                                                                       The present peptide is a chimaeric peptide (CP) contg. the Streptococcal M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)). The CP comprises a B-cell conformational epitope from within p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar conformation, enabling the epitope to be presented in an immunologically active conformation. The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised against the CP can be used for immunotherapy and diagnosis, while the CP can be used for immunotherapy and diagnosis, while the CP can be used so immunotherapy and signoresis, while the CP peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
                                                                                                                     New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines and for determn. of minimal epitope(s) or for mapping amphipathic helices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcal, M protein, peptide, p145; chimaeric, chimeric, B-cell, conformational epitope; alpha-hellx; GCN4; leucine zipper, detection; mapping, opsonic antibody, vaccine; group A Streptococci; immunotherapy, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/note= "pl45 conformational B-cell epitope"
                                                                                                                                                                                                                                                                                                                                                                                     / Match 91.2%; Score 125; DB 2; Length 28; Local Similarity 92.9%; Pred. No. 3e-08; nes 26; Conservative 2; Mismatches 0; Indels
COMMONWEALTH SCI & IND RES ORG.
UNIV MELBOURNE.
HALL INST MEDICAL RES WALTER & ELIZA.
BIOTECH AUSTRALIA PTY LID.
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                                                                        Saul AJ;
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                                                                                                                                                                   Example 12; Fig 1C; 99pp; English.
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                                                                        Good MF,
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                                                                       Cooper JA, Relf WA,
                                                                                               WPI; 1996-221939/22.
                                    (SIC-) BIOTECH (CSLC-) CSL LTD.
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Best Local Si
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW04354;
 (CSIR )
(UYME )
(HALL-)
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The present peptide is a chimaeric peptide (CP) contg. the Streptococcal M protein peptide p145 (Pruksakorn et al. J. Immunol. 149: 2729-2735 (1992)). The CP comprises a B-cell conformational peptide from within p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar conformation, enabling the epitope to be presented in an immunologically active conformation. The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised against the CP can be used for immunotherapy and diagnostic, while the CP can be used for immunotherapy and diagnostic, while the CP can be used so immunotherapy and diagnostic, while the CP can be used for immunotherapy and diagnostic, while the CP can be used for immunotherapy and diagnostic, while the CP can be used in a mean absorbance value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
                                                                                                                                                                                                                                                                                                   New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines and for determn. of minimal epitope(s) or for mapping amphipathic helices.
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/note= "p145 conformational B-cell epitope"
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Pred. No. 5.3e-08;
1; Mismatches 1; Indels
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HALL INST MEDICAL RES WALTER & ELIZA.
BIOTECH AUSTRALIA PTY LTD.
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BIOTECH AUSTRALIA PTY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 12; Fig 1C; 99pp; English.
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Best Local Similarity 92...
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The present peptide is a chimaeric peptide (CP) contg. the Streptococcal M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1929). The CP comprises a B-cell conformational peptode from within p145, inserted into a Deptide, pref. an alpha-helical coil based on the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar conformation, enabling the epitope to be presented in an immunologically active conformation. The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised against the CP can be used for immunotherapy and diagnostic. Ab raised can be used for immunotherapy and diagnostic, while the CP can be used so immunotherapy and seach diagnostically to detect Ab. The reactivity of the present peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
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                                                                                     New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines for determn. of minimal epitope(s) or for mapping amphipathic helices.
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/note= "p145 conformational B-cell epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 110; DB 2; Length 28;
Pred. No. 2e-06;
2; Mismatches 2; Indels
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    Saul AJ;
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                                                                                                                                                                          Example 12; Fig 1C; 99pp; English.
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  Good MF,
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  Cooper JA, Relf WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local 8
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(CSIR )
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Peptide
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                                                                                                                                                                                                                                                 The present peptide is a chimaeric peptide (CP) contg. the Streptococcal M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)). The CP comprises a B-cell conformational epitope from within p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on the GCN4 leucine zipper peptide, pref. an alpha-helical coil based on the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar active conformation, enabling the epitope to be presented in an immunologically active conformation. The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised against the CP can be used for immunotherapy and diagnosis, while the CP can be used diagnostically to detect Ab. The reactivity of the present peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
                                                                                                                        New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell; conformational epitope; alpha-helix; GCM4; leucine zipper; detection; mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy; diagnosis.
                                                                                                                                                                       for determn. of minimal epitope(s) or for mapping amphipathic helices.
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                                          Saul AJ;
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                                                                                                                                                                                                             Example 12; Fig 1C; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW04352 standard; protein; 28 AA.
                                        Good MF,
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                                        Relf WA,
                                                                                  WPI; 1996-221939/22
(CSLC-) CSL LTD.
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                                        Cooper JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW04352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CSIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ξê
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25-APR-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                AAR97454;
                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                AAR97454
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                                                                                                                                                                                                                                                                                                                 원
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                                                                                    The present peptide is a chimaeric peptide (CP) contg. the Streptococcal M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)). The CP comprises a B-cell conformational epitope from within p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on the GCN4 leucine zipper peptide (AAR971395). The 2nd peptide has a similar conformation, enabling the epitope to be presented in an immunologically active conformation. The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised against the CP can be used for immunotherapy and diagnosis, while the CP can be used diagnostically to detect Ab. The reactivity of the present peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
                   New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines and for determn. of minimal epitope(s) or for mapping amphipathic helices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper; detection; mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimaeric peptide (J4) contg. Streptococcal M protein peptide p145.
                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12. .23
/note= "p145 conformational B-cell epitope"
                                                                                                                                                                                                                                                                      70.1%; Score 96; DB 2; Length 28; 76.9%; Pred. No. 9.9e-05; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                         UNIV MELBOURNE.
HALL INST MEDICAL RES WALTER & ELIZA.
BIOTECH AUSTRALIA PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNCIL QUEENSLAND INST MEDICAL RES COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saul AJ;
                                                                                                                                                                                                                                                                                                                                 1 KOAEDKVKASREAKKOVEKALEOLED 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                  Example 12; Fig 1C; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               AAW04350 standard; protein; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Good MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-AU000681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94AU-00008851
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                  Best Local Similarity 76.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Relf WA,
WPI; 1996-221939/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-221939/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSL LTD.
                                                                                                                                                                                                                                                 Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9611944-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cooper JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW04350;
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CSIR )
(UYME )
(HALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CSPC-)
                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
AAW04350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines and for determn. of minimal epitope(s) or for mapping amphipathic helices.
New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines and for determn. of minimal epitope(s) or for mapping amphipathic helices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present peptide is a chimaeric peptide (CP), contg. a C. elegans unc-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paramyosin protein; peptide; unc-15; chimaeric; chimeric; B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper; detection; mapping; opsonic antibody; vaccine; immunotherapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimaeric peptide av86 contg. C. elegans unc-15 paramyosin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 81; DB 2; Length 40, Pred, No. 0.0065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CSIR ) COMMONWEALTH SCI & IND RES ORG.
(UYME ) UNIV MELBOURNE.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
(ERICT-) BIOTECH AUSTRALIA PTY LTD.
(CSLC-) CSL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES. (CSIR ) COMMONWEALTH SCI & IND RES ORG. (UYME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saul AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KQAEDDLDASREAKKQVQDKVKQLE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KOAEDKVKASREAKKOVEKALEQLE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 18; Page 44; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ż
                                                                                                                                            Example 12; Fig 1C; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR97454 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Good MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-AU000681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94AU-00008851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 68.v.,
Best Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-221939/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9611944-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-1995;
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The inventors claim a protein prod. by a strain of Gp.A Streptococci. The protein has the AA sequence of protein Habt lacks at least some part of the C and D regions (responsible for binding albumin), esp. it lacks the whole of these regions and extends for AAI to AAIS8. Compared with antural protein H, it is more specific and may be used as part of a kit for the binding, separation and identification of human IgG. The asme sequences appear in W09119741. (Updated on 27-AUG-2003 to correct os
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New IgG binding proteins H' lacking an albumin binding sequence in purificn. of excess IgG from blood and to diagnose autolmmune
                                                                                                                                                                                                                                                                               Protein H; immunoglobulin G; IgG; antibody; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 281;
                            110 DKVKEEKQISDASRQRLRRDLDASREAKKQVEKALEEANSKL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 DKVK------ASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bjorck L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72; DB 2;
Pred. No. 0.99;
2; Mismatches
                                                                                                                                                                                                                                             Sequence encoded by truncated M1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schmidt KH, Akesson P, Cooney J,
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 8; 37pp; English.
                                                                                                                          AAR20128 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                                                  1. .28
/label= p16M1
29. .70
/label= C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90SE-00002212
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Local Similarity 45.2%;
les 19; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= C2
113. .155
/label= C3
156. .176
/label= C4
                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177. .281
/label= D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HIGH-) HIGHTECH RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                    .112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-024366/03.
                                                                                                                                                                                                                                                                                                                   Streptococcus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-1990;
                                                                                                                                                                                             27-AUG-2003
15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9119740-A.
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                                                                                                                                                            AAR20128;
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                                                                                                                                                                                                                                                                                                                                                    Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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Matches
                                                                                                          AAR2012
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15 paramyosin peptide. The CP comprises a B-cell conformational epitope from within unc-15, inserted into a 2nd peptide, pref. an alpha-helical coll based on the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar conformation, enabling the epitope to be presented in an immunologically active conformation. The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against C. elegans. Ab raised against the CP can be used for immunotherapy and diagnosis, while the CP can be used diagnostically to detect Ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This M'6 protein corresponds to the conserved exposed polypeptide region of the streptococcal M protein. It is encoded by a gene- tically engineered gene introduced into the genome of a vaccinia or fewlpox virus. The resultant DMA complex is useful as a vaccine for immunoprotection against streptococcal infections. The M'6 polypeptide is the part of protein M responsible for virulence. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant streptococcal M protein DNA and viral vector - for production of poxviridae vaccines in treatment of vaccinia, fowlpox etc.
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcal M protein; M'6 protein; vaccinia virus; fowlpox virus; poxviridiae vaccine; streptococcal pharangytis.
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                                                                                                                                                                                                            Length 28;
                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                            ), DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.6%; Score 72; DB 2;
45.2%; Pred. No. 0.81;
tive 2; Mismatches
                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                            Score 78;
Pred. No.
                                                                                                                                                                                                                                                                           1 KOAEDKVKASREAKKQVEKALEQLE 25
                                                                                                                                                                                                                                                                                             AAR10221 standard; protein; 234 AA.
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                                                                                                                                                                                                          56.9%;
64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00369118
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90US-00540586,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNIV OREGON STATE.
                                                                                                                                                                                                      Query Match
Best Local Similarity 64.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcal M6' protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 45.2
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kruby DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-022236/03.
N-PSDB; AAQ10244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus sp
                                                                                                                                                                          Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fischetti VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9015872-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
26-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR10221;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide(s) from streptococcal M protein - used to prepare vaccines for providing protection against streptococcal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.6%; Score 72; DB 1; Length 441; Best Local Similarity 45.2%; Pred. No. 1.6; Matches 19; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                         Location/Qualifiers
216. .235
248. .269
275. .284
                      AAP90955 standard; protein; 441 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                          88US-00173380.
89US-00315588.
                                                                                                                                                                                                                                                                                                    89WO-US001026
                                                                                                                                                                   Stretococcus sp; 'group A'.
                                                                   27-AUG-2003 (revised)
25-MAR-2003 (revised)
23-FEB-1990 (first entry)
                                                                                                                     M6 streptococcal protein.
                                                                                                                                                                                                                                                                                                                                                             (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-309382/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 441 AA;
                                                                                                                                            Immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                      Fischetti VA;
                                                                                                                                                                                                                                                                                                                          25-MAR-1988;
27-FEB-1989;
                                                                                                                                                                                                                                                                                                   13-MAR-1989;
                                                                                                                                                                                                                                                    WO8909064-A.
                                                                                                                                                                                                                                                                           05-OCT-1989.
                                              AAP90955;
                                                                                                                                                                                                     Region
Region
Region
RESULT 15
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270 DKVKEEKQISDASRQGLRRDLDASREAKKQVEKAI

Search completed: August 4, 2005, 08:59:24 Job time : 164.209 secs

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6611666116661
Sequence 16, Appl
Sequence 67, Appl
Sequence 6, Appli
Sequence 12, Appl
Sequence 11, Appli
Sequence 11, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 66, Appl
Sequence 15, Appl
Sequence 17, Appli
Sequence 170, Appli
Sequence 170, Appli
Sequence 170, Appli
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                      August 4, 2005, 08:27:17; Search time 40.4651 Seconds (without alignments) 53.498 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                              /cgn2 6/ptodata/1/laa/5A_COMB.pep:*
/cgn2 6/ptodata/1/laa/5B_COMB.pep:*
/cgn2 6/ptodata/1/laa/6A_COMB.pep:*
/cgn2 6/ptodata/1/laa/6B_COMB.pep:*
/cgn2 6/ptodata/1/laa/FOTUS_COMB.pep:*
/cgn2 6/ptodata/1/laa/FOTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-817-811-18
US-08-817-811-17
US-08-817-811-16
US-08-817-811-16
US-08-102-756E-35
US-08-792-475-6
US-08-917-811-12
US-08-917-271-11
US-08-917-271-11
US-08-917-271-11
US-08-917-811-65
US-08-917-811-74
US-08-817-811-74
US-08-817-811-73
US-08-817-811-73
US-08-817-811-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-474-633A-92
US-08-823-771-92
PCT-US92-06412-105
US-08-817-811-13
                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                  US-10-706-275-2
137
1 KQAEDKVKASREAKKQVEKALEQLEDKVK
                                                                                                                                                                                              513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*
                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
APPLICANT: Relf, Wendy A.
APPLICANT: Saul, Allan J.
TITLE GOOG, WINCTABLIC PEPTIDES AND VACCINES
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
TITLE OF INVENTION: COMPRISING SAME
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS: ADDR
US-08-817-811-78
US-08-182-175A-57
US-08-423-771-75
US-08-823-771-75
US-08-182-175A-49
US-08-823-771-58
US-08-823-771-88
US-08-817-811-71
US-08-817-811-72
US-08-817-811-75
US-08-817-811-75
US-08-817-811-75
US-08-817-811-75
US-08-182-175A-85
                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/08817811
Patent No. 6174528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 28 amino acide
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.3
Best Local Similarity 85.2
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 512/474-7577
        97777788888866677776
      RESULT 1
US-08-817-811-18
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Length 28;
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                                                                                                                STATE: TAXAB

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE PORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997

CLASSIFICATION NUMBER: W0 96/11944

PRIOR APPLICATION NUMBER: W0 96/11944

FILING DATE: 25-APR-196
ATTONEY/AGENT INPORMATION:
REGISTRATION NUMBER: 37,642

REFERENCE/POCKET NUMBER: 37,642

REJEPRAN: $12/418-3000

TELEPRAN: $12/418-3000

TELEPRAN: SIZ/418-3000

TELEPRAN: SIZ/418-3000

TELEPRAN: OR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
APPLICANT: Realf, Wendy A.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES TITLE OF INVENTION: COMPRISING SAME NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: TEXAS

CONNTRY: USA

ZIP: 77210

COMPUTER TRADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/817,811

FILING DATE: 14-APR.1997

CLASSIFICATION 1424

PRIOR APPLICATION NUMBER: WO 96/11944

FILING DATE: 25-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 81; DB 3;
Pred. No. 0.0035;
4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KQAEDKVKASREAKKQVEKALEQLE 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-817-811-67
; Sequence 67, Application US/08817811
; Patent No. 6174528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.1%;
Best Local Similarity 68.0%;
Matches 17; Conservative
ADDRESSEE: Arnold, Wh:
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-817-811-16
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                                                                                                                                                                                                              Sequence 17, Application US/08817811
Fatent No. 6174528
Fatent Ralf, Wendy A.
FAPPLICANT: Relf, Wendy A.
FAPPLICANT: Good, Michael F.
APPLICANT: Good Michael F.
Fatent F.
Fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION NUMBER: WO 96/11944
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 77,422
REFERENCE/DOCKET NUMBER: FBRC:005
TELEPHONE: 312/414-7577
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: MINDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cooper, Juan A.
Relf, Wendy A.
Good, Michael F.
Saul, Allan SYNTHETIC PEPTIDES AND VACCINES
VVENTION: COMPRISING SAME
                                          2 KOAEDKVDASREAKKOVEKKVKQLEDK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KOAEDKVKASREAKKOVEKALEQLED 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08817811
Patent No. 6174528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SY
TITLE OF INVENTION: CO
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cooper,
APPLICANT: Relf, We
APPLICANT: Good, MI
APPLICANT: Saul, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-08-817-811-16
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Sequence 6. Application US/08325278B

Patent No. 6822075

GENERAL INFORMATION:

TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESSE: Seed IP Law Group

STREET: 701 Fifth Avenue Suite 6300

CITY: Seattle

STATE: Washington

CONTINT: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: SEATTH: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 DKVKEEKQISDASRQRLRRDLDASREAKKQVEKALEEANSKL 313
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,475
FILING DATE: IN-FEB-1997
CLASSIFICATION NUMBER: 33,963
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 100084.402D1
PELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                           : SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Potter, Jane B. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 100084.402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72; DB 2
Pred. No. 0.65;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278B
FILING DATE: 26-Oct-1994
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.2
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-795-475-6
           CORRESPONDENCE ADDRESS
                                                                                                                   CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-325-278B-6
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j Patent No. 673751

j GENERAL INFORMATION:
APPLICANT: FISCHETTI, Vincent A.
APPLICANT: POZZI, Gianni
APPLICANT: POZZI, Gianni
APPLICANT: SCRINEEWIND, Olaf
ITILE OF INVENTION: DELIVERY AND EXPRESSION OF A HYBRID SURFACE PROTEIN ON
ITILE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
FILE REFERENCE: 016921-076
CURRENT APPLICATION NUMBER: US 07/522,440
FRIOR APPLICATION NUMBER: US 07/522,440
FRIOR APPLICATION NUMBER: US 07/742,199
FRIOR PRILING DATE: 1991-08-05
FRIOR APPLICATION NUMBER: US 07/742,199
FRIOR APPLICATION NUMBER: US 07/814,823
FRIOR APPLICATION NUMBER: US 07/81,082
FRIOR APPLICATION NUMBER: US 07/81,082
FRIOR APPLICATION NUMBER: US 07/81,082
FRIOR APPLICATION NUMBER: P2133
FRIOR FILING DATE: 1993-03-13
FRIOR FILING DATE: P2091-08-05
FRIOR FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Patent No. 5965390
GENERAL INFORMATION:
APPLICANT: Bjvrck, Lare
APPLICANT: Sjvrzing, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 78; DB 3; Length 28;
Pred. No. 0.0077;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.6%; Score 72; DB 4;
Best Local Similarity 45.2%; Pred. No. 0.64;
Matches 19; Conservative 2; Mismatches
                               NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REPERENCE/DOCKET NUMBER: FBRC:005
TELEPHONE: 512/418-3000
TELEPACK: 512/418-3000
TELEPACK: 512/418-377
INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KOAEDKVKASREAKKQVEKALEQLE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KQAEDDLDASREAKKQLQDKVKQLE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 64.0%;
Matches 16; Conservative
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: S. pyogenes
US-08-302-756E-35
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-817-811-67
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LENGTH: 440
TYPE: PRT
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                                                                                                                                                                                                           Gaps
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                                                                                                                                                              52.6%; Score 72; DB 4; Length 443;
45.2%; Pred. No. 0.65;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 71; DB 3; Length 28; 55.6%; Pred. No. 0.049; ive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                        272 DKVKEEKQISDASRQRLRRDLDASREAKKQVEKALEEANSKL 313
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR.1997
CLASSIFICATION NUMBER: WO 96/11944
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: PBRC:005
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
TELEPHONE: 512/414-7577
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
APPLICANT: Relf, Wendy A.
APPLICANT: Sod, Michael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KOAEDKVKASREAKKQVEKALEQLEDK 27
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                   LENGTH: 443 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENUE DESCRIPTION: SEQ ID NO: 6:
US-08-325-278B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston STATE: Texas
COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08817811 Patent No. 6174528
SEQUENCE CHARACTERISTICS
                                                                                                                                             Query Match
Best Local Similarity 45.27
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Best Local Similarity 55.6
Matches 15; Conservative
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US-08-817-811-12
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RESULT 9

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Gaps
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APPLICANT: Dale, James B.

TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER TITLE OF INVENTION: FOR GROUP A STREPTOCCCCAL VACCINE FILE REFERENCE: 481112.404C2

CURRENT APPLICATION NUMBER: US/08/914,479A

CURRENT FILING DATE: 1997-06-19

PRIOR APPLICATION NUMBER: 08/409,270

PRIOR APPLICATION NUMBER: 07/945,860

PRIOR APPLICATION NUMBER: 07/945,860

PRIOR FILING DATE: 1992-09-16

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PSSEG for Windows Version 4.0

LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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                                                                          APPLICANT: Dale, James B.
APPLICANT: Lederer, James W.
TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/937,271

FILING DATE: 15-SEP-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Rosenman, Stephen J.

REGISTRATION NUMBER: 481112.405C1

TELECOMMUNICATION: PORMATION:

TELECOMMUNICATION: PORMATION:
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6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
Sequence 11, Application US/08937271
Patent No. 6063386
GENERAL INFORMATION:
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; Sequence 4, Application US/08914479A
; Patent No. 6419932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0%;
Matches 15; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-937-271-11
                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                              ADDRESSEE:
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ZIP: 77210

COMPUTER READABLE FORM:

MEDIUW TYEE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/817,811

FILING DATE: 14-APR-1997

CLASSIFICATION NUMBER: WO 96/11944

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO 96/11944

FILING DATE: 25-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: H1901ANGE: 37,642

REGISTERATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: FBRC:005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
TITLE OF INVENTION: COMPRISING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 68.5; DB 3;
Pred. No. 0.096;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 3
Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
       NAME: Rosenman, Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 481112.405C1
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 66, Application US/08817811; Patent No. 6174528; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 ASREAKKQVEKALEEANSKL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.0%;
Best Local Similarity 55.2%;
Matches 16; Conservative '
                                                                                                                                                                               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   LENGTH: 305 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-271-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-817-811-66
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US-08-817-811-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08914479A
; Sequent No. 6419932
; GENERAL INFORMATION:
; TILLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
; FILE REPERENCE: 481112.404C2
; CURRENT APPLICATION NUMBER: US/08/914,479A
; FILE REPRENCE: 48112.404C2
; CURRENT PILING DATE: 1997-08-19
; PRIOR PELICATION NUMBER: 09/409,270
; PRIOR FILING DATE: 1995-03-23
; PRIOR FILING DATE: 1995-09-16
; NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.8%; Score 71; DB 4; Length 284; Best Local Similarity 75.0%; Pred. No. 0.53; Matches 15; Conservative 2; Mismatches 3; Indels
                                                                              DB 4; Length 254;
                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08937271
Patent No. 6063386
GENERAL INFORMATION:
APPLICANT: Dale, James B.
APPLICANT: Lederer, James W.
TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Columbia Center, 701 Fifth Avenue STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: Washington COUNTRY: USA ZIP: 98104
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMpatible COMPUTER: IBM PC COMpatible COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS COMPATING SYSTEM: PC-DOS/M
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,271
FILING DATE: 15-SEP-1997
                                                                       Query Match 51.8%; Score 71; DB 4; Best Local Similarity 75.0%; Pred. No. 0.48; Matches 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                        105 ASREAKKOVEKALEEANSKI 124
                                                                                                                                                                                                                     9 ASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 ASREAKKOVEKALEEANSKL 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-08-914-479A-6
US-08-914-479A-4
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LENGTH: 284
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48.9%; Score 67; DB 3; Length 29;
Best Local Similarity 48.3%; Pred. No. 0.15;
Matches 14; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                      Sequence 52, Application US/08817811

Patent No. 6174528

GENERAL INFORMATION

APPLICANT: Relf, Wendy A. APPLICANT: Good, Michael F. APPLICANT: Good, Michael F. APPLICANT: Good, Michael F. APPLICANT: Saul, Allan J. TITLE OF INVENTION: COMPRISING SAME NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS: 97

CORPUTER: Texas

COUNTRY: USA

STATE: Texas

COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: SPECHER PCOSS/WS-DOSS/WS-DOSS/PCOMPUTER: DEFENTION COMPUTER: COMPUTE
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APPLICANT: Cooper, Juan A.
APPLICANT: Cooper, Juan A.
APPLICANT: Real, Walchael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES TITLE OF INVENTION: COMPRISING SAME
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTONNEY/ABORNT INFORMATION:
KQAEDKVKASREAKKQVEKALEQLEDKVK 29
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Patent No. 6174528
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REGISTRATION NUMBER: 37,642
REFRENCE/DOCKET NUMBER: PBRC:
TELECOMMUNICATION INFORMATION:
TELEPAX: 512/418-300
TELEPAX: 512/418-307
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS:
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US-08-817-811-52
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US-08-817-811-15
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ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 443

CITY: Housen

STATE: Texas

CONNETT: Texas

CONNETTE: Texas

COMPUTER: Texas

COMPUTE
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us-10-706-275-2.rapb

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Sequence 10, Appl
Sequence 9, Appli
Sequence 6, Appli
Sequence 672, App
Sequence 3295, Ap
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Sequence 15, Appl
Sequence 12, Appl
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                                                                                                                                                                                                   August 4, 2005, 08:36:38; Search time 141.628 Seconds (without alignments)
. 79.939 Million cell updates/sec
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Sequence 14,
Sequence 11,
Sequence 10,
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22: /cgn2_6/ptodata/1/pubpaa/US108_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 US-10-706-275-15

US-10-706-275-12

US-10-706-275-13

US-10-706-275-14

US-10-706-275-11

US-10-706-275-10

US-10-706-2
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137
1 KQAEDKVKASREAKKQVEKALEQLEDKVK 29
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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86.9
81.8
80.3
70.1
59.1
52.6
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Perfect score:
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1137
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                                                                                                                                                                                                               Run on:
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No.
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12 71 51.8 254 13 US-10-141-627-4 Sequence 4, Appli  
14 65.5 47.8 18 18 108-10-141-627-6 Sequence 67.45.  
15 65.5 47.8 13 US-10-0-146-675-5 Sequence 67.45.  
16 64 67.7 12 US-10-706-275-8 Sequence 12, Appli  
17 64 46.7 20 13 US-10-706-275-5 Sequence 22, Appli  
18 64 67.7 20 13 US-10-706-275-5 Sequence 23, Appli  
18 64 67.7 20 17 US-10-706-275-5 Sequence 24, Appli  
19 63 46.0 107 17 US-10-706-275-5 Sequence 27, Appli  
20 62 45.3 77 14 US-10-706-275-5 Sequence 97, Appli  
21 62 45.3 77 14 US-10-706-275-5 Sequence 97, Appli  
22 62 45.3 77 14 US-10-706-275-5 Sequence 97, Appli  
23 61 44.5 28 17 US-10-706-275-5 Sequence 97, Appli  
24 61 41.5 28 17 US-10-706-275-5 Sequence 97, Appli  
25 61 44.5 37 71 US-10-804-678-92 Sequence 97, Appli  
26 61 44.5 37 71 US-10-804-678-92 Sequence 97, Appli  
27 61 44.5 37 71 US-10-804-678-95 Sequence 97, Appli  
28 61 44.5 37 71 US-10-804-678-95 Sequence 97, Appli  
29 61 44.5 37 71 US-10-804-678-95 Sequence 97, Appli  
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20 61 44.5 97 71 US-10-804-678-97 Sequence 97, Appli  
21 60 43.8 42 14 US-10-23-0664-34 Sequence 97, Appli  
22 62 43.8 49 17 US-10-804-678-34 Sequence 97, Appli  
23 60 43.8 49 17 US-10-804-678-34 Sequence 97, Appli  
24 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 60 43.8 6
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US-10-706-275-2

Sequence 2, Application US/10706275

Sequence 2, Application US/10706275

Sequence 2, Application US/10706275

Sequence 2, Application Wo. US20050002956A1

SEQUENCE CONTROWARTION:

APPLICANT: The Council of the Queensland Institute of Medical Research APPLICANT: The Council of the Queensland Institute of Medical Research APPLICANT: Burt, David S.

APPLICANT: Burt, David S.

APPLICANT: Batzloff, Michael F.

APPLICANT: Batzloff, Micha
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OTHER INFORMATION: antigenic peptide derivative of S. pyogenes with flanking sequen-OTHER INFORMATION: es

Length 29

Score 137; DB 17; Pred. No. 7.8e-09;

100.0%;

Query Match Best Local Similarity

JS-10-706-275-2

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Gapa

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Matches

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APPLICANT: ID Biomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: Good, Michael F.
APPLICANT: Batzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ID Biomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: He Council of the Queensland Institute of Medical Research
APPLICANT: Burt, David S.
APPLICANT: Withe, Gregory L.
APPLICANT: Good, Michael F.
APPLICANT: Batzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
                                       ; THER.INFORMATION: antigenic peptide sequence derivative of p145 base US-10-706-275-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THER INFORMATION: antigenic peptide sequence derivative of p145 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 28;
                                                                                                                                      Length 28;
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                                                                                                                                                                                           0; Indels
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86.9%; Score 119; DB 17;
Best Local Similarity 89.3%; Pred. No. 8.3e-07;
Matches 25; Conservative 2; Mismatches 1;
                                                                                                                                Score 125; DB 17;
Pred. No. 1.7e-07;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFTILE OF INVENTION: Vaccine
FILE REFERENCE: 021999-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/426,409
PRIOR APPLICATION NUMBER: N 2002302132
PRIOR APPLICATION NUMBER: AU 2002302132
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 13
                                                                                                                                                                                                                                              1 KQAEDKVKASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                   1 KOAEDKVKASREAKKÓVEKAVKOLEDKV 28
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FILE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 60/426,409
PRIOR FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/10706275 Publication No. US20050002956A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/10706275
Publication No. US20050002956A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                      91.2%;
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                Query Match
Best Local Similarity 92.99
Matches 26; Conservative
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US-10-706-275-14
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APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: Good, Michael R.
APPLICANT: Barzloff, Michael R.
APPLICANT: Barzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
TITLE OF INVENTION: Vaccine
FILE REPERENCE: 201999-00071008
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
                                                                                                                                                                                                               %30-706-275-15

// Sequence 15, Application US/10706275

// Sequence 15, Application US/10706275

// Publication No. US20050002956A1

// APPLICANT: ID Biomedical Corporation of Quebec

// APPLICANT: ID Biomedical Corporation of Quebec

// APPLICANT: Lowell, George H.

// APPLICANT: Burt, David S.

// APPLICANT: Burt, David S.

// APPLICANT: Bartle, Gregory L.

// APPLICANT: Bartlef, Michael R.

// APPLICANT: Landerson, Tomas B.

// TITLE OF INVENTION: Vaccine

// TITLE OF INVENTION: Vaccine
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           Gaps
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Best Local Similarity 100.0%; Pred. No. 7.8e-09;
Matches 29; Conservative 0; Mismatches 0;
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     0; Mismatches
                                                                                                             1 KOAEDKVKASREAKKOVEKALEQLEDKVK 29
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PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: AU 2002302132
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/706,275 CURRENT FILING DATE: 2003-11-13
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PRIOR APPLICATION NUMBER: US 60/426,409
PRIOR FILING DATE: 2002-11-15
PRIOR FILING DATE: 2002-11-15
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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ORGANISM: Artificial Sequence
        29; Conservative
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LENGTH: 28
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GENERAL INFORMATION
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APPLICANT: ID Blomedical Corporation of Quebec
APPLICANT: The Council of the Queengland Institute of Medical Research
APPLICANT: The Council of the Queengland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: Good, Michael R.
APPLICANT: Leanderson, Tomas B.
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
FILE REPERENCE: 021989-007108
CURRENT PILING DATE: 2003-11-13
PRIOR PLLING DATE: 2002-11-15
PRIOR PLLING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/426,409
PRIOR PLING DATE: 2002-11-15
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
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Publication No. US20050002956A1
GENERAL INFORMATION:
APPLICANT: ID Blomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: Good, Michael R.
APPLICANT: Batzloff, Michael R.
                                                                                                                                                                                           FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-14
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81.8%; Score 112; DB 17; Length 28;
Best Local Similarity 88.9%; Pred. No. 5.2e-06;
Matches 24; Conservative 1; Mismatches 2; Indels
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Pred. No. 8.7e-06;
2; Mismatches 2;
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PRIOR APPLICATION NUMBER: AU 2002302132
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Publication No. US20050002956A1
                    PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 28
                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 85.2%;
Matches 23; Conservative ·
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Publication No. US20050002956A1
GENERAL INFORMATION:
APPLICANT: ID Biomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: White, Michael F.
APPLICANT: Batzloff, Michael F.
APPLICANT: Batzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 0.017;
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TITLE OF INVENTION: Vaccine
FILE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
PRIOR PILING DATE: 2002-11-15
PRIOR FILING DATE: 2002-11-15
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SERVING NO 10
LENGTH: 28
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THIE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
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PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: AU 2002302132
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
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; Publication No. US20030027283A1
                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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68.0%;
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Best Local Similarity 68.0v
Best Local 17; Conservative
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; ORGANISM: Streptococcus pyogenes US-10-732-923-3295
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APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE S: 14
CORRESPONDENCES: ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
CONTRY: USA
ITP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: RADAPLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BREPE PATENTON DATE: 26-OCT-1996
CURRENT APPLICATION NUMBER: US/08/325,278
FILING DATE: 26-OCT-1996
CLASSIFICATION NUMBER: 45-0023.401
FELECOMMUNICATION NUMBER: 45-0023.401
FELECOMMUNICATION NUMBER: 45-0023.401
FELECOMMUNICATION NUMBER: 43-963
REFERENCE/DOCKET NUMBER: 45-0023.401
FELECOMMUNICATION NOS 6: SEQUENCE CHARACTERSTICNS
INFORMATION FOR SEQ ID NO: 6: SEQUENCE TYPE: protein
US-08-325-278-6
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Publication No. US20040236072A1
GENERAL INFORMATION:
APPLICANT: Olmsted, Stephen
APPLICANT: Inickbarg, Robert
APPLICANT: Nickbarg, Elliot
APPLICANT: Winter, Lourie
TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
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l Similarity 45.2%; Pred. No. 4.3;
19; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.6%; Score 72; DB 8; Length 443; 45.2%; Pred. No. 3.4; tive 2; Mismatches 3; Indels
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CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
LENGTH: 553

// TYPE: PRT
// ORGANISM: Streptococcus pyogenes
US-10-474-792-672

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Best Local Similarity 45.2
Matches 19; Conservative
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Matches 19; Conserv
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Sequence 3295, Application US/10732923

Publication No. US2050108791A1

GENERAL INFORMATION:

APPLICANT Edgerton, Michael D

TITLE OF INVENTION: TANGEBRIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFRENCE: 38-15(52796)C

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2003-12-10

PRIOR FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149
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Publication No. US20020176863A1

FUBLICANT: Dale, James B.

TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER

TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE

TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE

FILE REFERENCE: 481112.40423

CURRENT APPLICATION NUMBER: US/10/141,627

CURRENT FILING DATE: 2002-05-07

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 254

TYPE: PRT

CURRENT ARTIFICIAL Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.6%; Score 72; DB 17; Length 558; Best Local Similarity 50.0%; Pred. No. 4.3; Matches 18; Conservative 3; Mismatches 7; Indels
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Publication No. US20020176863A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dale, James B.
TITLE OF INVENITION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
FILE REPERRNCE: 481112.404G3
CURRENT APPLICATION NUMBER: US/10/141,627
CURRENT APPLICATION NUMBER: US/2007
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FRAESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: An antigen of MS and a carrier of the OTHER INFORMATION: COOH-terminal portion of M5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 KQTSDASRQGLRRDLDASREAKKQVEKALEEANSKL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KQAED-----KVKASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 ASREAKKQVEKALEEANSKL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 ASREAKKOVEKALEQLEDKV 28
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TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                           FEATURE:
OTHER INFORMATION: An antigen of three fragments of M5 and a carrier
OTHER INFORMATION: of the COOH-terminal portion of M5
US-10-141-627-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                Query Match 51.8%; Score 71; DB 1
Best Local Similarity 75.0%; Pred. No. 2.8;
Matches 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE REPERENCE: INCRMITICALION OF EBBERILLE
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT PILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/200, 848
FRIOR PILING DATE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/200, 848
FRIOR APPLICATION NUMBER: 60/200, 848
FRIOR APPLICATION NUMBER: 60/200, 848
FRIOR APPLICATION NUMBER: 60/200, 335
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-09
FRIOR PELING DATE: 2000-05-09
FRIOR APPLICATION NUMBER: 60/230, 335
FRIOR APPLICATION NUMBER: 60/242, 578
FRIOR PILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/242, 578
FRIOR APPLICATION NUMBER: 60/245, 591
FRIOR APPLICATION NUMBER: 60/253, 625
FRIOR APPLICATION NUMBER: 60/253, 625
FRIOR APPLICATION NUMBER: 60/253, 636
FRIOR APPLICATION NUMBER: 60/257, 931
FRIOR APPLICATION NUMBER: 60/257, 931
FRIOR APPLICATION NUMBER: 60/257, 931
FRIOR PILING DATE: 2000-11-22
FRIOR APPLICATION NUMBER: 60/257, 931
FRIOR PILING DATE: 2001-02-09
FRIOR PILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-282-122A-67145
Sequence 67145, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Haelbeck, Robert
APPLICANT: Haelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Paslind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 ASREAKKQVEKALEEANSKL 154
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US-10-282-122A-67145
                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
SEQ ID NO 6
LENGTH: 284
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APPLICANT:
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Sequence 8, Application US/10706275;
Publication No. US20050002956A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: ID Blomedical Corporation of Quebec
APPLICANT: Lowell, George H.
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: White, Gregory L.
APPLICANT: Burt, David S.
FULE REFERENCE: 021989-000710US
TITLE OF INVENTION: Vaccine
FILE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT APPLICATION NUMBER: US/60/426,409
FRIOR APPLICATION NUMBER: US 60/426,409
FRIOR APPLICATION NUMBER: AU 2002302132
FRIOR APPLICATION NUMBER: AU 2002302132
FRIOR APPLICATION NUMBER: AU 2002302132
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47.8%; Score 65.5; DB 17;
Best Local Similarity 58.6%; Pred. No. 0.99;
Matches 17; Conservative 2; Mismatches 3;
1 KQAEDKVKASREAKKQVEKALEQLEDKVK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KQAERDLDASREAKK------QLQDKVK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: August 4, 2005, 08:55:14 Job time : 142.628 sec8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 15
SOFWARE: Patentin version 3.1
SEQ ID NO B
LENGTH: 28
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

August 4, 2005, 08:50:19; Search time 31.6977 Seconds (without alignments) 88.028 Million cell updates/sec Run on:

1 KQAEDKVKASREAKKQVEKALEQLEDKVK 29 US-10-706-275-2 137 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	gamm	TO TO	protein M precurso	M protein precurso	plasminogen-bindin	plasminogen-bindin	M6 protein - Strep	M1 protein precurs	protein	•••	M protein precurso	M protein - Strept	M protein precurso	M5 protein precurs	M24 protein precur	IgG-binding protei	hypothetical prote			conserved hypothet	hypothetical prote	probable zuotin [i	beta-tropomyosin -	alanine-tRNA ligas	tropomyosin beta c	tropomyosin 1, emb	tropomyosin 1, fib	tropomyosin beta,	
SUMMARIES		ei ei	JC1419	A49545		S30284			A26297	S35401		S34978				A28616	A28549	S57835	T45031	T45039	G75219	H64327	T22180	T50972	S23470	AF0843	TWRBB	TMRTF1	A23562	S00922	A44131
		Length DB		388 2	•	•	454 2	•	483 2	484 2		484 2		532 2	•	492 2	539 2	528 2	1365 2	1408 2	217 2	104 1	493 2	445 2	284 2	876 2	284 1	284 1	284 2	284 2	284 2
d	Query	Match Length	52.9	52.6	52.6	52.6	52.6	52.6	52.6	52.6	52.6	52.6	52.6	52.6	ä	51.8	51.8	51.1	48.2	48.2	46.7	46.4	٠	•	43.8	43.8	43.1	43.1	43.1	43.1	43.1
	,	Score	72.	72	72	72	72	72	72	72	72	72	72	72	72	71	71	70	99	99	9	63.5	62	61	9	9	59	59		59	29
	Result	. No.	rt	7	Ю	4	ហ	ø	7	8	σ'n	10.	11	12	13	14	15	16	17	18		20	21	22	23	24	25		27	28	29

-	tropomyosin beta,	tropomyosin beta -	tropomyosin beta,	cell wall binding	hypothetical prote	tropomyosin 1, smo	tropomyosin 1, ske	hypothetical prote	myosin heavy chain	conserved hypothet	hypothetical prote	general stress pro	tropomyosin, fibro	tropomyosin 5 - mo	tropomyosin isofor	tropomyosin - rat	
	S03838	S23256	B25073	AH1387	B71203	TMCHS1	A30125	T34490	A26655	D70449 .	E97357	AI1274	A25530	S11390	S34124	153784	
	~	N	~	~	7	н	~	7	~	7	~	~	~	7	~	~	
	284	284	284	436	217	284	284	751	2116	558	169	174	248	248	248	248	
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	43	43	43	43	42.3	42	42	42	42	42	41	41	41	41	41	41	
	59	29	83	29	28	28	28	28	28	57.5	57	57	57	57	57	57	
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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RESULT 1
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Fc gamma (1gG) receptor II precursor - Streptococcus sp. N;Alternate names: fcrV protein

C;Species: Streptococcus sp.
C;Species: Streptococcus sp.
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1419; S17354
C;Accession: JC1419; B17354
Gene 120, 27-32, 1992
A;Atille: Protein V, a novel type-II IgG receptor from Streptococcus sp.: Sequence, homol A;Reference number: JC1419; MUID:93013016; PMID:1398120

A;Molecule type: DNA A;Rebidues: 1-837 <SM1-3 A;Cross-references: UNIPROT:Q55312; EMBL:X62467; NID:g47562; PIDN:CAA44324.1; PID:g4756⁻ A;Experimental source: strain 22/58'Valente'

Gyguerfamily: MS protein
Cysuperfamily: MS protein
Cysuperfamily: MS protein
Cykeywords: duplication; immunoglobulin receptor
Cyteywords: duplication; immunoglobulin receptor
Cyteywords: duplication; immunoglobulin receptor
Cyteywords: duplication; immunoglobulin receptor
Fy14-268/Pegion: 35-residue repeat A
Fy16-303/Region: 35-residue repeat A
Fy174-408/Region: 35-residue repeat B
Fy14-408/Region: 35-residue repeat B
Fy16-450/Region: 35-residue repeat B

13; Score 72.5; DB 2; Length 587; Pred. No. 2.5; Indels 9 19; Conservative Best Local Similarity Query Match Matches

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Gaps

417 KVKEDKQISDASRQGLRRDLDASREAKKQVEKALEEANSKL 457 1 KQAEDK-------VKASREAKKQVEKALEQLEDKV 28 ઠે 셤

plasminogen-binding protein PAM precursor - Streptococcus pyogenes (fragment) N.Alternate names: plasminogen-binding M-like protein (Pd 53) C;Species: Streptococcus pyogenes C;Species: Streptococcus pyogenes C;Accession: A49545; SG1084; SG0829; S70459; S32619 Ext_change 09-Jul-2004 C;Accession: A49545; SG1084; SG0829; S70459; S32619 A;Berge, A.; Sjoebring, U. A;Berge, A.; Sjoebring, U. A;Reference number: A497-244, 1933 A;Reference number: A49545; MUID:94064605; PMID:8244975 A;Molecule type: DNA A;Residues: 1-388

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A;Residues: 1.436 <POD1>
A;Cross-references: UNIRROT:Q54839; EMBL:X58179
A;Cross-references: UNIRROT:Q54839; EMBL:X58179
Fyedbielski, A.; Melzer, B.
submitted to the EMBL Data Library, February 1991
A;Description: Pcr mediated cloning and sequencing of group A streptococcal emm41/52 (ev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vir regulon in group A streptococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CiSpecies: Streptococcus sp.
CiActer 14-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999
CiAccession: 845598; 843556
Riben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebring, U.
Riben Sachem. 222, 267-226, 1994
A;Title: Streptokinase activates plasminogen bound to human group C and G streptococci
A;Reference number: 845598; MUID:94291620; PMID:8020466
                                                                                                                                                                                                                                                                                                                                                                       M protein precursor - Streptococcus pyogenes (serotype M52)
C;Species: Streptococcus pyogenes
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S30284; S29681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-454 <BE2>
A;Crose-references: EMBL:232677; NID:g474767; PIDN:CAA83589.1; PID:g474768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-216,'N',218-436 <POD2>
A;Cross-references: EMBL:X58179; NID:g47364; PIDN:CAA41168.1; PID:g47365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 454;
                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ASREAKKQVEKALEQLEDKV 28
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Mol. Gen. Genet. 237, 287-300, 1993
A;Title: Three different types of organization of the vi
A;Reference number: $30283; MUID:93204905; PMID:8455563
A;Accession: $30284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: transmembrane protein
C;Keywords: transmembrane protein
F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-436/Product: M protein #status predicted <MAT>
F;411-429/Domain: transmembrane #status predicted <TVM>
                                                                                                                                                                        1 KQAED-----KVKASREAKKQVEKALEQLEDKV 28
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2.2;
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                            ed. No. 2;
Mismatches
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Pred. No.
                         50.0%; Pred. No.
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A;Molecule type: DNA
                                                             3,
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1 Similarity 45.2%;
19; Conservative 5
                                                             18; Conservative
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A;Accession: S29681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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les 19; Conserv
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Best Local Similarity
Matches 19; Conserv
                            Best Local Similarity
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A; Molecule type: DNA
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                                                             Matches
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A;Cross-references: UNIPROT:P49054; EMBL:Z22219; NID:g288978; PIDN:CAA80222.1; PID:g9408
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
a) Description: Noncongruent relationships between variation in emml gene sequences and the A;Reference number: $61072
A;Reference number: $61072
A;Residues: 13-96 A;Reserence servicype MS3
A;Residues: 13-96 A;Repur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
A;Residues: 13-96 A;Repur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
A;Residues: 13-96 A;Repur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
A;Residues: 13-96 A;M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
A;Residues: 11-77 A;Residues: S60784; MUID:9519837; PMID:7891551
A;Residues: 17-77 A;Residues:
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C.Specias: Streptococcus pyogenes
C.Specias: Streptococcus
C.Specias: Streptococcus
C.Specias: Streptococcus
A; Title: Three different types of organization of the vir regulon in group A streptococcc
A; Reference number: Streptococcus
A; References: UNIPROT: CS4837; EMBL:X58178
A; Residues: 1-408 <- Poptococcus
C.Specialski, A.; Melzer, B.
Bubmitted to the EMBL Data Library, February 1991
A; Reference number: Streptococcal emm41/52 (ev
A; Reference number: Streptococcal emm41/52 (ev
A; Reference number: Streptococcal emm41/52 (ev
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A; Residues: 1-230, 'N', 232-371,'R',373-408 <POD2>
A; Cross-references: EMBL:X58178; NID:g47362; PIDN:CAA41167.1; PID:g47363
C; Genetics:
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Pred. No. 1.9;
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C;Reywords: transmembrane protein
F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-408/Product: M protein #status predicted <MAT>
F;383-401/Domain: transmembrane #status predicted <TMM>
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larity 45.2%;
Conservative
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19; Conserv
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Query Match

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A,Residues: 16-94 <WHA>
A,Residues: 16-94 <WHA>
A,Cross-references: EMBL:U11940; NID:g533557; PIDN:AAA99556.1; PID:g533558
A,Cross-references: EMBL:U11940; NID:g533557; PIDN:AAA99556.1; PID:g533558
Mol. Microbiol. 14, 619-631, 1994
A,Title: Non-congruent relationships between variation in emm gene sequences and the poly.
A,Reference number: S60784; MUID:95198537; PMID:7891551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S46489; S46490 Ts;Acsession: Schmidt, K.H.; Cooney, J.; Bjoerck, L. Biochem. J. 300, 877-886, 1994
A;Title: Mi protein and protein H: IgGFc- and albumin-binding streptococcal surface prot. A;Reference number: S46489; MUID:94280417; PMID:8010973
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C;Species: Streptococcus pyogenes
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: 834978; 831966
R;Harbaugh, M.P.; Podbielski, A.; Huegl, S.; Cleary, P.P.
Mol. Microbiol. 8, 981-991, 1993
A;Title: Nucleotide substitutions and small-scale insertion produce size and antigenic v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Streptococcus pyogenes
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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A,Experimental source: strain 40/58, serotype M1
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C;Keywords: transmembrane protein
E;1-41/Domain: signal sequence #status predicted <SIG>
F;42-484/Product: M1 protein #status experimental <MAT>
F;459-477/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 29-89 <WH2> A;Cross-references: EMBL:U11940
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Pred. No. 2.4;
2; Mismatches
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A;Residues: 42-51 <AKW>
A;Experimental source: strain 40/58, serotype
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Best Local Similarity 45.2%;
Matches 19; Conservative
A; Reference number: S61072
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                                                                            A;Status: preliminary A;Molecule type: DNA
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M6 protein - Streptococcus pyogenes
C; Species: Streptococcus pyogenes
C; Species: Streptococcus pyogenes
C; Species: Streptococcus pyogenes
C; Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C; Accession: A26297
R; Hollingshead, S.K.; Fischetti, V.A.; Scott, J.R.
J. Biol. Chem. 261, 1677-1686, 1986
A; Title: Complete nucleotide sequence of type 6 M protein of the group A streptococcus.
A; Reference number: A26297; MUID:86111835; PMID:3511046
A; Accession: A26297
A; Molecule type: DNA
A; Residues: 1-483 <a href="https://document.com/">Holloward</a>
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: M5 protein
C; Keywords: coiled coil; transmembrane protein
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S35401
MI procein precursor - Streptococcus pyogenes
C; Species: Streptococcus pyogenes
C; Species: Streptococcus pyogenes
C; Species: Streptococcus pyogenes
A; Variety: serotype MI
C; Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C; Accession: 335401; S61074; S60784
R; Pobbielski, A.
submitted to the EMBL Data Library, September 1991
A; Recession: S35401
A; Molecule type: DNA
A; Recession: S35401
A; Molecule type: DNA
A; Residues: 1-484 < PDA
A; Residues: 1-484 < PDA
A; Residues: UNIPROT: Q10372; EMBL: X62131; NID: G311757; PIDN: CAA44062.1; PID: G3117
B; Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A; Description: Noncongruent relationships between variation in emml gene sequences and the constant of the
                                                                                                                                                C; Species: Streptococcus sp.
A; Variety: group G
C; Accession: S4559; S43554
E; Arcession: S4559; S43554
E; Bur. J. Biochem. 222, 267-276, 1994
A; Title: Streptokinase activates plasminogen bound to human group C and G streptococci
A; Reference number: S45598; WUID:94291620; PMID:8020466
A; Accession: S45598
A; Accession: S45598
A; Residues: 1-472
A; Residues: EmBL: Z32678; NID:g474769; PIDN:CAA83389.1; PID:g1333838
C; Superfamily: M5 protein
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                                                                                                              plasminogen-binding protein MLG72 - Streptococcus sp. (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 2; Length 472;
Pred. No. 2.3;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72; DB 2; Length 483;
Pred. No. 2.4;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 DKVKEEKQISDTSRKGLRRDLDASREAKKOVEKALEEANSKL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 DKVK-----ASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKVK-------ASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 52.6%;
Local Similarity 45.2%;
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.2%;
Matches 19; Conservative
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Best Local S
Matches 19
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Score 72; DB 2
Pred. No. 2.7;
2; Mismatches
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                                                                                                                                                                                52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.6%;
Best Local Similarity 45.2%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: translation not shown
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                                                                                                                                                                       Query Match
Best Local Similarity 45.23
Matches 19; Conservative
                                                                                                                                                                                                                                                                                           5 DKVK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S61072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 13-111 <WHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-564 <ROB>
                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A40174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S61072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
A44643
M protein precursor - Streptococcus pyogenes (serotype M57) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M57
C;Date: 26-58p-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C;Accession: A44643; S60833
C;Accession: A44643; S60833
C;Accession: A44643; S60833
A;Title: Hepted motifs within the distal subdomain of the coiled-coil rod region of M pr.
A;Accession: A44643 MUID: 92143933; PMID: 1781883
A;Accession: A44643; MUID: 92143933; PMID: 1781883
A;Accession: A44643
A;Etatus: preliminary
A;Residues: 1-501 <AMAN>
A;Experimental source: type M57, strain A995
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence inconsistent with nucleotide (translation of the sequences and the pop A;Note: parts of this sequence were confirmed by peptide sequencing
A;Note: parts of this sequence were confirmed by peptide sequences and the pop A;Itle: Non-congruent relationships between variation in emm gene sequences and the pop A;Reterus: precliminary; nucleic acid sequence not shown; translation not shown
A;Reference number: S34978; MUID:93360826; PMID:8355619
A;Accession: S34978
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-484 <HAR>
A;Acsion: S1484 <HAR>
A;Cross-references: UNIPROT:Q05464; EMBL:Z21845; NID:g49401; PIDN:CAA79893.1; PID:g49402
C;Genetics:
A;Gene: emml.1
C;Genetics:
C;Superfamily: MS protein
C;Keywords: membrane protein
F;1-42/Domain: signal sequence #status predicted <SIG>F;1-42/Domain: signal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL Data Library, July 1994
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S54871
M protein - Streptococcus sp.
C;Species: Streptococcus sp.
C;Species: Streptococcus sp.
C;Species: S54871
R;Podbielski, A.; Melzer, B.
R;Podbielski, A.; Melzer, B.
R;Podbielski, A.; Melzer, B.
R;Ripodbielski, A.; Melzer, B.
R;Ripodbielski, A.; Melzer, B.
R;Ripodbielski, A.; Melzer, B.
R;Ripodpielski, A.; Melzer, B.
R;Ripodpielski, A.; Melzer, B.
R;Ripodpielski, A.; Melzer, B.
R;Ripodpielski, A.; Melzer, B.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                               DB 2; Length 484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 DKVKEEKQISDASRQGLRRDLDASREAKKQVEKALEEANSKL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 DKVKEEKQISDASRQGLRRDLDASREAKKQVEKALEEANSKL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was submitted to the
                                                                                                                                                                                                                                                                                                                                            Query Match 52.6%; Score 72; DB 2
Best Local Similarity 45.2%; Pred. No. 2.4;
Matches 19; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 2
Pred. No. 2.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.6%;
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A;Note: the nucleotide sequence v
C;Superfamily: MS protein
C;Keywords: coiled coil; dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 DKVK-----
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Best Local Similarity 45.2
Matches 19; Conservative
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A,Molecule type: DNA
A,Residues: 1-532 <POD>
A,Cross-references: UNIPROT:Q55098; EMBL:X60097; NID:g840905; PIDN:CAA42693.1; PID:g8409
C,Superfamily: M5 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Wolecule type: protein
A;Residues 42-54 «KRA»
A;Residues 42-54 «KRA»
R;Chen, C.; Bormann, N.; Cleary, P.P.
Mol. Gen. Genet. 241, 685-693, 1993
Mol. Gen. Genet. 241, 685-693, 1993
A;Title: VirR and Mry are homologous trans-acting regulators of M protein and C5a peptid.
A;Reference number: S39886; MUID:94088463; PMID:7505389
A;Accession: S39887
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R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the popi A;Reference number: S60784; MUID:95198537; PMID:7891551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Streptococcus pyogenes
C; Species: Streptococcus pyogenes
C; Date: 08 Dec-1992 #sequence revision 08-Dec-1992 #text_change 09-Jul-2004
C; Date: 08 Dec-1992 #sequence revision 08-Dec-1992 #text_change 09-Jul-2004
C; Accession: A40174; A60115; S39887; S61072; S60793
R; Robbins, J.C.; Spanier, J.G.; Jones, S.J.; Simpson, W.J.; Cleary, P.P.
A; Title: Streptococcus pyogenes type 12 M protein gene regulation by upstream sequences.
A; Reference number: A40174; MUID:88058777; PMID:2445730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:M18269; NID:g153543; PIDN:AAA88573.1; PID:g153544
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A;Molecule type: DNA
A;Residuss: 1-15 «CHE»
R;Whatmore, A.; Kepur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
Submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emml gene sequences and
                                                                                                                                                                                                                                                                    ä
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                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein precursor - Streptococcus pyogenes (serotype M12) (fragment)
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                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                         Length 532;
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F;42-564/Product: M protein (fragment) #status predicted <MAT>
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                                                                                                                                                                                         DB 2;
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Pred. No. 2.6;
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2; Mismatches

15; Conservative

Matches

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Job time : 32.6977 secs
                                       390 ASREAKKQVEKALEEANSKL 409
9 ASREAKKQVEKALEQLEDKV 28
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A; Residues: 1-492 kML)

A; Residues: 1-492 kML)

A; Crose references: UNIPROT: P02977; GB:M20374; NID:g153812; PIDN: AAA26976.1; PID:g153813

R; Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.

Mol. Microbiol. 14, 619-631, 1994

A; Title: Non-congruent relationships between variation in emm gene sequences and the pop A; Reference number: $60784; MUD:9519837; PMID:7891551

A; Reference number: $60784; MUD:95198537; PMID:7891551

A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra A; Molecule type: DNA

A; Status: preliminary; nucleic acid sequence not shown; not compared conceptual tra A; Residues: 30-89 kMA>

C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: M5 protein
C; Keywords: coiled coil; transmémbrane protein
C; Keywords: coiled coil; transmémbrane protein
C; Keywords: coiled coil; transmémbrane predicted <MAT>
F; 43-492/Product: M5 protein #status predicted <MAT>
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A; Redidues: 1-539 <MOLD.
A; Redidues: 1-539 <MOLD.
A; Cross-references: UNIPROT: P12379; GB:M19031; NID:g153616; PIDN:AAA26874.1; PID:g153617
A; Cross-references. A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A; Title: Non-congruent relationships between variation in emm gene sequences and the pop
A; Reference number: S60784; MUID:95198537; PMID:7891551
                                                                                                                                                         A28616

Sprotein precursor - Streptococcus pyogenes

C;Species: Streptococcus pyogenes

A;Variety: serotype M5

C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004

C;Accession: A28616; S60787

R;Miller, L.; Gray, L.; Beachey, E.; Kehoe, M.

A;Title: Autigenic variation among group A streptococcal M proteins. Nucleotide sequence

A;Reference number: A28616; MUID:88186881; PMID:3281944
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A28549
A28549
A28549
A28549
A28549
A2 Preptrococcus pyogenes
C;Species: Streptococcus pyogenes
C;Species: Streptococcus pyogenes
A;Variety: serotype M24
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A28549; B.H.; Burdett, V.
A; Beachey, E.H.; Burdett, V.
A; Bacteriol. 170, 676-684, 1988
A;Title: Molecular evolution of streptococcal M protein: cloning and nucleotide sequence
A;Reference number: A28549; MUID:88115166; PMID:3276665
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A;Molecule type: DNA
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                        405 DKVKEEKQISDASROGLRRDLDASREAKKOVEKALEEANSKL 446
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Pred. No. 3.3;
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C,Superfamily: MS protein
C,Keywords: coiled coil; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 ASREAKKÖVEKALEEANSKL 362
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Matches 15; Conserv
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Best Local Similarity
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OM protein

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Sequence:

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RX SUCHEACE FOLCH

RA COllins C.M., Kimura A., Bisno A.L.;

RA Collins C.M., Kimura A., Bisno A.L.;

RT "Group G streptococcal m protein exhibits structural features

RT "Group G streptococcal m protein of group A streptococci.";

RIL Infect. Immun. 60:3689-3696(1992).

CC -- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by

RA COLO09986; C.cell wall: EA.

BR GO; GO:0009986; C.cell wall; EA.

BR GO; GO:0005086; C.cell wall; IEA.

BR GO; GO:0016020; C.membrane; IEA.

BR GO; GO:0016020; C.membrane; IEA.

BR GO; GO:0016020; C.membrane; IEA.

BR HITEFPRO; IPRO01899; Gram_pos anchor.

BR HITEFPRO; IPRO01899; Gram_pos anchor.

BR Fam; PF00450; YSIRK signal; 1.

BR FAM; PF00450; YSIRK signal; 1.

BR TIGRFAMB; TIGRO1169; XSIRK signal; 1.

BR TIGRFAMB; TIGRO1169; XSIRK signal; 1.

BR TIGRFAMB; TIGRO1169; XSIRK signal; 1.

BR TIGRFAMB; TIGRO1169; ASIRK signal; 1.

BR TIGRFAMB; TIGRO1169; ASIRK signal; 1.

BR TIGRFAMB; TIGRO1169; SYSIRK signal; 1.
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                     QSS279
P08089
Q00374
Q00372
Q54830
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Q55098
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Q54718
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Q88599
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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46.3%; Pred. No. 16;
ive 4; Mismatches
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Q99XV0
Q99XV0
Q54830
Q54830
Q76MJ2
Q55098
Q55098
M12_STRPY
Q54718
M12_STRPY
Q5485P9
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M6_STRPY
Q05464
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                                             7000000
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les 19; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1320;
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Q00720
ID Q00720
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Q840T7
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                                                                                                                                                    August 4, 2005, 08:38:38; Search time 153.767 Seconds (without alignments) 96.576 Million cell updates/sec
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Q54703
Q55278
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                            US-10-706-275-2
137
1 KQAEDKVKASREAKKQVEKALEQLEDKVK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                             1612378 segs, 512079187 residues
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Maximum Match 100%
Listing first 45 summaries
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Q671K5
Q671K5
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Q8G1B0
Q8G1A4
Q8G1A4
Q8G1A4
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Q8G1A1
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Q8G1A1
                                                                                                         - protein search, using sw model
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Q9AMM3
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Q54640
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Perfect score:
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Minimum DB 1 Maximum DB 1

Database

Result ģ

Searched:

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-!-- SUBCELLUIAR LOCATION: Attached to the cell wall peptidoglycan by an anide bond (By similarity).

EMBL; X62467; CAA44324.1; -.

PIR; JC1419; JC1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Сарв
                                                                                                                                                                                                                                                                                                MEDLINE=93013016; PubMed=1398120; DOI=10.1016/0378-1119(92)90005-A;
                                                                                                                                                                                                                                                                                                       Smirnov O.Y., Denesyuk A.I., Zakharov M.V., Abramov V.M., Zav'yalov V.P., Ponesyuk A.I., Zakharov M.V., Abramov V.M., Protein V. P., Protein Protein V. a novel type-II IgG receptor from Streptococcus sequence, homologies and putative Fc-binding site."; Gene 120:27-32(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Straptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                          Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein V.
; D9FA5658AC23FA81 CRC64;
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                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%; Score 72.5; D
46.3%; Pred. No. 25;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0015; GPOSANCHOR.
TIGRFAMS; TIGR01167; LPXTG anchor; 1.
TIGRFAMS; TIGR01168; VSTRK signal; 1.
TIGRFAMS; TIGR01168; VSTRK signal; 1.
Cell wall; Peptidoglycan-anchor; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, O15813, 1D7M.
GO, GO:0005986, C:cell surface, IEA.
GO, GO:0005618, C:cell wall, IEA.
GO, GO:001520, C:membrane, IEA.
InterPro; IPR001897, Gpos YSIRK.
InterPro; IPR01899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; Pfam; PF00746; Gram_pos_anchor; Pfam; PF00770; M, I.
Pfam; PF04550; YSIRK signal; 1.
                                                                                              PRT;
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Best Local Similarity 46.39
Matches 19, Conservative
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                                                                                             PRELIMINARY;
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                                                                                                                                                                  Protein V precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 587 AA;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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NCBI_TaxID=1314;
[1]
                                                                                                                                                                                             Streptococcus sp.
                                                                                                                                                                                                                                        NCBI_TaxID=1306;
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MEDLINE=95172752; PubMed=7868273;
MEDLINE=95172752; PubMed=7868273;
Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
"Generic diversity and relationships among Streptococcus pyogenes
strains expressing serotype MI protein: recent intercontinental spread
of a subclone causing episodes of invasive disease.";
Infect. Immun. 63:994-1003(1995).
EMBL; U20102; AAA85115.1; -.
EMBL; U20101; AAA85115.1; -.
EMBL; U20101; AAA85114.1; -.
EMBL; U20101; AAA85115.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Podbielski A., Baird R., Kaufhold A.;
The group A streptococcal M-type 3 protein gene exhibits a C terminus typical for class I M proteins.";
Med. Microbiol. Immunol. 181:209-213(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                Length 100;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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100 AA; 11345 MW; 9773331C00EDC2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 DKVKEEKQISDASRQGLRRDLDASREAKKÖVEKALEEANSKL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 AA; 21550 MW; A738888D947155D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                Score 72; DB 2;
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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TIGREAMS, TIGRO1167; LPXTG anchor; 1.
PROSITE; PS50847; GRAM POS ANCHORING; 1.
Cell wall; Peptidoglycan-anchor.
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Best Local Similarity 45.2
Matches 19, Conservative
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Streptococcus.
NCBI_TaxID=1314;
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Q54832;
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Q54832
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       Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
"Genetic diversity and relationships among Streptococcus pyogenes
strains expressing serotype MI protein: recent intercontinental spread
of a subclone causing episodes of invasive disease.";
Infect. Immun. 63:994-1003[1995].
EMBL: U20104; AAA85117.1;
HSSP: P13276; IEQ1.
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                                                                                                                                                                                                                                                                                                   Query Match 52.6%; Score 72; DB 2; Length 100; Best Local Similarity 45.2%; Pred. No. 5.9; Matches 19; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 100;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MI protein (Fragment).
Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                               100 AA; 11243 MW; 9775831FA25DC463 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                ----ASREAKKQVEKALEQLEDKV 28
                                                                                                                                                                                                                                                                                                                                                                                                                    28 DKVKEEKQISDASRQGLRRDLDASREAKKQVEKALEEANSKL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 AA; 11287 MW; 9773331914EDC2D3 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.6%; Score 72; DB 245.2%; Pred. No. 5.9; iive 2; Mismatches
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MEDLINE=95172752; PubMed=7868273;
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InterPro; IPR003345; M_repeat.
Pfam; PF02370; M; 1.
                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
InterPro; IPR003345; M_repeat.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 45.2
Matches 19; Conservative
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SEQUENCE FROM N.A.

STRAIN=M nontypeable group A;

Brandt E.R., Good M.F.;

Submitted (Aug-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (Aug-1996) to the EMBL/GenBank/DDBJ databases.

- I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).

EMBL, UGSB99; ABAB40640.1; ---

CO, GO:0005618; C:cell surface; IEA.

GO; GO:0005618; C:cell wall; IEA.

RO; GO:0005618; C:cell wall; IEA.

GO; GO:0005618; C:cell wall; IEA.

RO; GO:0005618; C:cell wall; IEA.

RO; GO:0005618; Gram_pos anchor.

RICHEPPO: IPR001345; M repeat.

REAM; PF00146; Gram_pos_anchor; 1.

REAMS; PR0015; GPOSANCHOR.

TIGREAMS; TIGROIL67; LPXTG_anchor; 1.

REAMS; TIGROIL67; LPXTG_anchor; 1.

ROSITE; PS50847; GRAM POS_ANCHORING; 1.

ROSITE; PS50847; GRAM POS_ANCHORING; 1.

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NON_TER 2.08

SEQÜENCE 2.08 AA; 22695 MW; 013FBBABOA97FF42 CRC64;
                                        Gaps
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                                     3; Indels
                                                                                                                                                                                                                                                                                                                           P95824;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-2097 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
M protein (Fragment).
Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
M procein (Fragment)
Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                               ----ASREAKKQVEKALEQLEDKV 28
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45.2%; Pred. No. 11.
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   Best Local Similarity 45.2 Matches 19; Conservative
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Best Local Similarity 45.2
Matches 19; Conservative
                                                                                            5 DKVK------
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NCBI_TaxID=1314;
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Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shetzigovsky I., Ravins M., Korenman Z., Cohen-Poradosu R., Nir-Paz R., emm typing of M nontypeable invasive group A streptococcal isolates in Israel., I. Microbiol. 41:4655-4659(2003).

EMBL; AY394538; AA094530-1; -. GO; GO:0016020; C:membrane; IEA.

InterPro; IPR003345; M_repeat.

Pfan: PF02370; M; I. 1

NON_TER
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA; 22565 MW; 79972A987324729B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: ::|:
172 KEEQNKISEASRKGLRRDLDASREAKKQVEKALEEANSKL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGTLR5;
0-5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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ilarity 42.5%; Pred. No. 13;
Conservative 6; Mismatches
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GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016020; C:membrane; IEA.
InterPro; IRR01899; Gram pos_anchor.
InterPro; IRR01345; M repeat.
Pfam; PF00716; Gram pos_anchor; 1.
Pfam; PF02370; M; 1.
PRINTS; PR00015; GPOSANCHOR.
TIGRRAM; TIGR01167; LPXTG_anchor; 1.
PROSITE; PS0847; GRAM POS_ANCHORING; 1.
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last seq
05-UUL-2004 (TrEMBLrel. 27, Last ann
M protein (Fragment).
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MEDLINE=22894607; Pubmed=14532198;
                                                                                                                                                                                                                                                                                                                                                                Local Similarity 45.2 nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                      208
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[1]
SEQUENCE FROM N.A.
Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
McMillan D.;
                                                                                                                                                                                                     Query Match 52.6%; Score 72; DB 2; Length 282; Best Local Similarity 45.2%; Pred. No. 15; Matches 19; Conservative 2; Mismatches 3; Indels
                                                        Submitted (Aug-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX139401; AAN64674.1; -.
Co; Go:0016020; Cmembrane; IEA.
InterPro; IRRO03345; M_repeat.
PFam; PF02770; M; 1.
NON_TER 1 1
NON_TER 282 282
SEQÜENCE 282 AA; 32157 MW; 5C799B0AA4323541 CRC64;
                                                                                                                                                                                                                                                                 5 DKVK-------ASREAKKQVEKALEQLEDKV 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus.
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                                                        STRAIN-JSB;
MOSEB A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shtzigovsky I.,
Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shtzigovsky I.,
Ravins M., Korenman Z., Cohen-Poradosu R., Nir-Paz R.;
Submitted (JUL-2013) to the EMBL/GenBank/DDBJ databases.
EMBL, AY346386; AAQ72206.1;
GQO; GO:0016020; C:membrane; IEA.
InterPro; IPR00324; M_repeat.
PF02370; M: 1.
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                                                                                                                                                                                                                                              Query Match 52.6%; Score 72; DB 2; Length 251; Best Local Similarity 45.2%; Pred. No. 13; Matches 19; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 52.6%; Score 72; DB 2; Length 279; Local Similarity 45.2%; Pred. No. 15; Lonservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                              199 DKVKEEKQISDASRQGLRRDLDASREAKKQVEKALEEANSKL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY139420; AAN64693.1; -. G.; GO; GO: Co: C:membrane; IEA. InterPro; IFR003345; M_repeat. PF02370; M; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 DKVKEEKOISDASROGLRRDLDASREAKKOVEKALEBANSKL 243
                                                                                                                                                                                                   251 251
251 AA; 28938 MW; 2A66602AAA637D11 CRC64;
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279 AA; 31224 MW; 16A600455BC5C3A0 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
M protein (Fragment).
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Name=emm;
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                                              SEQUENCE FROM N.A.
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                NCBI_TaxID=1314;
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Q8GL87
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                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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204 DKVKBEKQISDASRQGLRRDLDASREAKKQVEKALEEANSKL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 303
303 AA; 34562 MW; F76F37540E16CD1B CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
M protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 KOVSDASROGLRRDLDASREAKKOVEKALEBANSKL 265
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